

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 05:38:57 : Search time 1793 Seconds  
(without alignments)  
7841.542 Million cell updates/sec

Title: US-09-787-677A-7  
Perfect score: 2742  
Sequence: 1 agaaagcagcgcgcgcagaga.....ggatcacaataatcgtcagc 2742

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 3: /cgn2\_6/prodata/1/pubpna/US05\_PUBCOMB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US04\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US03\_PUBCOMB.seq:\*
- 6: /cgn2\_6/prodata/1/pubpna/US02\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/1/pubpna/US01\_PUBCOMB.seq:\*
- 8: /cgn2\_6/prodata/1/pubpna/US00\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/1/pubpna/US05\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodata/1/pubpna/US04\_PUBCOMB.seq:\*
- 15: /cgn2\_6/prodata/1/pubpna/US03\_PUBCOMB.seq:\*
- 16: /cgn2\_6/prodata/1/pubpna/US02\_PUBCOMB.seq:\*
- 17: /cgn2\_6/prodata/1/pubpna/US01\_PUBCOMB.seq:\*
- 18: /cgn2\_6/prodata/1/pubpna/US00\_PUBCOMB.seq:\*
- 19: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 20: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 21: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2715	99.0	2863	15	US-10-301-822-23
2	1482.8	54.1	1918	9	US-09-988-598-2589
3	1472	53.7	1475	10	US-09-888-257A-1
4	1472	53.7	1475	10	US-09-946-374-133
5	1472	53.7	1475	13	US-10-006-867-79
6	1472	53.7	1475	13	US-10-063-547-79
7	1472	53.7	1475	13	US-10-063-551-79
8	1472	53.7	1475	14	US-10-028-072-491
9	1472	53.7	1475	14	US-10-063-616-79
10	1472	53.7	1475	14	US-10-140-808-491
11	1472	53.7	1475	14	US-10-063-569-79
12	1472	53.7	1475	14	US-10-063-513-79

13	1472	53.7	1475	14	US-10-063-515-79	Sequence 79, Appl
14	1472	53.7	1475	14	US-10-063-512-79	Sequence 79, Appl
15	1472	53.7	1475	14	US-10-121-049-491	Sequence 491, Appl
16	1472	53.7	1475	14	US-10-123-904-491	Sequence 491, Appl
17	1472	53.7	1475	14	US-10-140-470-491	Sequence 491, Appl
18	1472	53.7	1475	14	US-10-063-502-79	Sequence 79, Appl
19	1472	53.7	1475	14	US-10-175-746-491	Sequence 491, Appl
20	1472	53.7	1475	14	US-10-176-918-491	Sequence 491, Appl
21	1472	53.7	1475	14	US-10-176-921-491	Sequence 491, Appl
22	1472	53.7	1475	14	US-10-063-549-79	Sequence 79, Appl
23	1472	53.7	1475	14	US-10-137-865-491	Sequence 491, Appl
24	1472	53.7	1475	14	US-10-140-474-491	Sequence 491, Appl
25	1472	53.7	1475	14	US-10-142-419-491	Sequence 491, Appl
26	1472	53.7	1475	14	US-10-142-431-491	Sequence 491, Appl
27	1472	53.7	1475	14	US-10-143-114-491	Sequence 491, Appl
28	1472	53.7	1475	14	US-10-140-002-491	Sequence 491, Appl
29	1472	53.7	1475	14	US-10-063-554-79	Sequence 79, Appl
30	1472	53.7	1475	14	US-10-006-856A-133	Sequence 133, Appl
31	1472	53.7	1475	14	US-10-142-419-491	Sequence 491, Appl
32	1472	53.7	1475	14	US-10-063-553-79	Sequence 79, Appl
33	1472	53.7	1475	14	US-10-123-265-491	Sequence 491, Appl
34	1472	53.7	1475	14	US-10-142-423-491	Sequence 491, Appl
35	1472	53.7	1475	14	US-10-063-598-79	Sequence 79, Appl
36	1472	53.7	1475	14	US-10-227-693-79	Sequence 79, Appl
37	1472	53.7	1475	14	US-10-006-818A-133	Sequence 133, Appl
38	1472	53.7	1475	14	US-10-121-050-491	Sequence 491, Appl
39	1472	53.7	1475	14	US-10-141-755-491	Sequence 491, Appl
40	1472	53.7	1475	14	US-10-143-032-491	Sequence 491, Appl
41	1472	53.7	1475	14	US-10-063-563-79	Sequence 79, Appl
42	1472	53.7	1475	14	US-10-006-485A-133	Sequence 133, Appl
43	1472	53.7	1475	14	US-10-013-907A-133	Sequence 133, Appl
44	1472	53.7	1475	14	US-10-015-499A-133	Sequence 79, Appl
45	1472	53.7	1475	14	US-10-063-555-79	Sequence 79, Appl

#### ALIGNMENTS

RESULT 1  
US-10-301-822-23  
Sequence 23, Application US/10301822  
Publication No. US20030148410A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kamackar, Shubhang  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MEMO-0292RNM  
CURRENT APPLICATION NUMBER: US/10/301,822  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 2863  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (231)...(923)  
US-10-301-822-23

Query Match 99.0%; Score 2715; DB 15; Length 2863;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGAGTATGAGGTGTTCAAGAGCAGA 60  
DB 113 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGAGTATGAGGTGTTCAAGAGCAGA 172  
QY 61 GCTTCAGCCTGAGAGCAGAGGAGAGTCCCTGAAGAGGCTTCTAAGAGGTGTCAT 120  
DB 173 GCTTCAGCCTGAGAGCAGAGGAGAGTCCCTGAAGAGGCTTCTAAGAGGTGTCAT 232  
QY 121 GGCCTCTCTTGGCCTCCCAACTTGTGGGCTACATCTAGAGCCTTCTGGGAGC 180  
DB 233 GGCCTCTCTTGGCCTCCCAACTTGTGGGCTACATCTAGAGCCTTCTGGGAGC 292  
QY 181 ACTGTTGCGATGCTGCTCCCAAGCTGAGAAACAGATTCTTATGTGGTGCAGCATTT 240  
DB 293 ACTGTTGCGATGCTGCTCCCAAGCTGAGAAACAGATTCTTATGTGGTGCAGCATTT 352  
QY 241 GACAGCAGTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCGCAGACAGAGCAT 300  
DB 353 GACAGCAGTGGCTTCTCCAAAGGCTCTGGATGGAATGTGCGCAGACAGAGCAT 412  
QY 301 CACCCAGTGTGACATCTATAGCACCCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 360  
DB 413 CACCCAGTGTGACATCTATAGCACCCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 472  
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 473 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 532  
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
DB 533 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 592  
QY 481 TGGAGTCTTTTTCATCTCTGGAGGCTCTGGAGTTCATCTCTGGAGTTCATCTCT 540  
DB 593 TGGAGTCTTTTTCATCTCTGGAGGCTCTGGAGTTCATCTCTGGAGTTCATCTCT 652  
QY 541 TGGAGTCTCTAAGGAGCTTCTAATCAACAATGATGATGATGATGATGATGATGATG 600  
DB 653 TGGAGTCTCTAAGGAGCTTCTAATCAACAATGATGATGATGATGATGATGATGATG 712  
QY 601 AGAGGCTCTTAACTGGGCAATTAATTTCTCCCTGTTCCCTGATGATGATGATGAT 660  
DB 713 AGAGGCTCTTAACTGGGCAATTAATTTCTCCCTGTTCCCTGATGATGATGATGAT 772  
QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTACCAAGCCA 720  
DB 773 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTACCAAGCCA 832  
QY 721 ACCTCTTGGCAGAGAGCTCTCCAGAGGCTGATCAATCTCCAAAGTCAAGAGTGT 780  
DB 833 ACCTCTTGGCAGAGAGCTCTCCAGAGGCTGATCAATCTCCAAAGTCAAGAGTGT 892  
QY 781 CAATTCCTAAGGCTGACAGGATATGTGTAAGAACAGAGGCTGAGGCTGAGGCTGAG 840  
DB 893 CAATTCCTAAGGCTGACAGGATATGTGTAAGAACAGAGGCTGAGGCTGAGGCTGAG 952  
QY 841 TGGGCTGTGTAAGAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATG 900  
DB 953 TGGGCTGTGTAAGAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATG 1012  
QY 901 GATTCGTGTGTAAGAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATG 960  
DB 1013 GATTCGTGTGTAAGAGAGTGTGCTGAGAGATGATGATGATGATGATGATGATGATG 1072  
QY 961 GCAAGAAATGGGGCTGATGTAAGAGATGATGATGATGATGATGATGATGATGATG 1020  
DB 1073 GCAAGAAATGGGGCTGATGTAAGAGATGATGATGATGATGATGATGATGATGATG 1132

QY 1021 CAGCCTTTCTGTTTCTCACTGCTGCTCCCTGCGCTTAAGTCCCAACCTCAACTT 1080  
DB 1133 CAGCCTTTCTGTTTCTCACTGCTGCTCCCTGCGCTTAAGTCCCAACCTCAACTT 1192  
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGCTCAAGAGATCCCTTGGCTCTGTTTAACTGGG 1140  
DB 1193 GAAACCCCATTTCCCTTAAGCAGAGCTCAAGAGATCCCTTGGCTCTGTTTAACTGGG 1252  
QY 1141 ACTTCATCCCAACCAATCAATCAATCCCACTGACCTCTGTGATCAAGACC 1200  
DB 1253 ACTTCATCCCAACCAATCAATCAATCCCACTGACCTCTGTGATCAAGACC 1312  
QY 1201 TCTCTGCTGAGTGGTGGCTCTTAAGTCAATGCTGGGATGAGAAAGAGACAGTGGC 1260  
DB 1313 TCTCTGCTGAGTGGTGGCTCTTAAGTCAATGCTGGGATGAGAAAGAGACAGTGGC 1372  
QY 1261 TTTTGTGGGATGCTCTTAACCTTCTCAACTTCCCTCCAAAGAACTGATTTGGCCC 1320  
DB 1373 TTTTGTGGGATGCTCTTAACCTTCTCAACTTCCCTCCAAAGAACTGATTTGGCCC 1432  
QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCCACAGTGCAGACTAATTTGTGATGAA 1380  
DB 1433 TGGAACTCCATCCCACTCTTGTATGACTCCACAGTGCAGACTAATTTGTGATGAA 1492  
QY 1381 CTGAAATTAACCATCTCTACGATATCCAGGAAACAGAAACAGATGAGAGTGGAGGA 1440  
DB 1493 CTGAAATTAACCATCTCTACGATATCCAGGAAACAGAAACAGATGAGAGTGGAGGA 1552  
QY 1441 CAGAAAGCAGCTGGGACATTTTAAAAATTAATAATGAAAAAACCAGAACCCATT 1500  
DB 1553 CAGAAAGCAGCTGGGACATTTTAAAAATTAATAATGAAAAAACCAGAACCCATT 1612  
QY 1501 TCTCAGGACCTTCTCAGAAATCTCTCAATTTGTGGGCTGGGATCAAGCTCAGACTTG 1560  
DB 1613 TCTCAGGACCTTCTCAGAAATCTCTCAATTTGTGGGCTGGGATCAAGCTCAGACTTG 1672  
QY 1561 AGAAAGCAGAAAGAAAGAAAGAAAGATCTGTGAAAGCTCAGTGGACGGAATCTG 1620  
DB 1673 AGAAAGCAGAAAGAAAGAAAGAAAGATCTGTGAAAGCTCAGTGGACGGAATCTG 1732  
QY 1621 ACTTCATGAGAACTGCTCAGAACTGAGATCAACAATTTGGCTGAAGCCCTGCTTC 1680  
DB 1733 ACTTCATGAGAACTGCTCAGAACTGAGATCAACAATTTGGCTGAAGCCCTGCTTC 1792  
QY 1681 ACTCTAGGACCTGACCTGAGCTCTTGGCTTAACCAAGAGCTAAGGCTATAGCAAT 1740  
DB 1793 ACTCTAGGACCTGACCTGAGCTCTTGGCTTAACCAAGAGCTAAGGCTATAGCAAT 1852  
QY 1741 GATTTCTTAAGAAAGATAACAGATTTTCTAAGGATGAGCTCTGGGAGATGACA 1800  
DB 1853 GATTTCTTAAGAAAGATAACAGATTTTCTAAGGATGAGCTCTGGGAGATGACA 1912  
QY 1801 GTGTGGAGCTGTGGGCTACTGAGAAAGACCAATTCCTTGAAGGTGTCTAAGAACCA 1860  
DB 1913 GTGTGGAGCTGTGGGCTACTGAGAAAGACCAATTCCTTGAAGGTGTCTAAGAACCA 1972  
QY 1861 GTGATGT 1920  
DB 1973 GTGATGT 2032  
QY 1921 AGAACTCTTCAAGGCTTAAGAAATCAAGCTCAATGAGATCAGGCCCCCAGGGTCC 1980  
DB 2033 AGAACTCTTCAAGGCTTAAGAAATCAAGCTCAATGAGATCAGGCCCCCAGGGTCC 2092  
QY 1981 ACCCAAGAGCACTAAGAGCTCTGAAAGACATAGCACCAAGGAGCCCTTCAGATT 2040  
DB 2093 ACCCAAGAGCACTAAGAGCTCTGAAAGACATAGCACCAAGGAGCCCTTCAGATT 2152  
QY 2041 CCCCACGTGCTCAAGGAGATGCTCAGAGTGGCTGAGAGGCACTTAAGGGCTCCAGCA 2100  
DB 2153 CCCCACGTGCTCAAGGAGATGCTCAGAGTGGCTGAGAGGCACTTAAGGGCTCCAGCA 2212  
QY 2101 TGGCATATCATGCCCCAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160



QY 1141 ACTTCATCCCAACCCATTAATCATATCCCACTGACTGACCTCTGTGATCAAAAGACC 1200  
DB 1542 ACTTCATCCCAACCCATTAATCATATCCCACTGACTGACCTCTGTGATCAAAAGACC 1601  
QY 1201 TCTCTGCTGAGTGGTGGCTCTTAAGCTCAATGCTGGGAGATGGGAAGAGAGAGTGGC 1260  
DB 1602 TCTCTGCTGAGTGGTGGCTCTTAAGCTCAATGCTGGGAGATGGGAAGAGAGAGTGGC 1661  
QY 1261 TTTTGTGGGAGTGGCTCTTAAGCTCTCAAGCTTCCCTCCCAAGAACTGATTTGGCCC 1320  
DB 1662 TTTTGTGGGAGTGGCTCTTAAGCTCTCAAGCTTCCCTCCCAAGAACTGATTTGGCCC 1721  
QY 1321 TGGAACTCCATCCCACTCTTTTATGACTTCACAGTTCACAGTCAATTTGTGATGAA 1380  
DB 1722 TGGAACTCCATCCCACTCTTTTATGACTTCACAGTTCACAGTCAATTTGTGATGAA 1781  
QY 1381 CTGAAATTAACCATCTTACGATATCGAGGAAGAGAAAGAGATGAGAGAGAGAGAG 1440  
DB 1782 CTGAAATTAACCATCTTACGATATCGAGGAAGAGAAAGAGATGAGAGAGAGAGAG 1841  
QY 1441 CAGGAAGCAGCCTGAGCAATTTAAAAAATAAAAATGAAAAAACCAGAA 1494  
DB 1842 CAGGAAGCAGCCTGAGCAATTTAAAAAATAAAAAATGAAAAAACCAGAA 1895

## RESULT 3

US-09-888-257A-1

Sequence 1, Application US/0988257A

Publication No. US2003060612A1

GENERAL INFORMATION:

APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Smith, Victoria  
APPLICANT: Wood, William I.  
APPLICANT: Wu, Thomas D.

APPLICANT: Zhang, Zhen

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TITILE OF INVENTION: TREATMENT OF TUMOR

FILE REFERENCE: P5002R1

CURRENT APPLICATION NUMBER: US/09/888,257A

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/063,540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: US 60/089,653

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 60/099,792

PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: US 60/103,678

PRIOR FILING DATE: 1998-10-08

PRIOR APPLICATION NUMBER: US 60/235,451

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: PCT/US99/12252

PRIOR FILING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: PCT/US99/20111

PRIOR FILING DATE: 1999-09-01

PRIOR APPLICATION NUMBER: PCT/US00/04342

PRIOR FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US01/06520

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: PCT/US01/06666

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 1  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-888-257A-1

Query Match 53.7%; Score 1472; DB 10; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGTGTTCAGAGAGAGAG 60  
DB 4 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGTGTTCAGAGAGAGAG 63  
QY 61 GCTTCAAGCTGGAAG 120  
DB 64 GCTTCAAGCTGGAAG 123  
QY 121 GGCCTCTCTTGGCTCCAACTTGTGGGCTACATCTAGGCTTTCTGGGCTTTTGGGAC 180  
DB 124 GGCCTCTCTTGGCTCCAACTTGTGGGCTACATCTAGGCTTTCTGGGCTTTTGGGAC 183  
QY 181 ACTGTTGCGATGCTGCTCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
DB 184 ACTGTTGCGATGCTGCTCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
QY 241 GACAGAGTGGCTTCTCCAGAGGCTCTGATGATGATGATGATGATGATGATGATGAT 300  
DB 244 GACAGAGTGGCTTCTCCAGAGGCTCTGATGATGATGATGATGATGATGATGATGAT 303  
QY 301 CACCAGTGTGATCTATATGACACCTTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 360  
DB 304 CACCAGTGTGATCTATATGACACCTTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 363  
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423  
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
QY 481 TGGAGTCTTTTATCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATCTTCA 540  
DB 484 TGGAGTCTTTTATCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATCTTCA 543  
QY 541 TGGAGTCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATTCATCTTGTGCTGAG 600  
DB 544 TGGAGTCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATTCATCTTGTGCTGAG 603  
QY 601 AGAGGCTCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATTCATCTTGTGCTGAG 660  
DB 604 AGAGGCTCTTGAAGGCTCTGAGATTCATCTTGTGCTGAGATTCATCTTGTGCTGAG 663  
QY 661 CTGCTTTCTGCTGATCCAGAGAAATGCTTCAACTACTACTACTACTACTACTACTACT 720  
DB 664 CTGCTTTCTGCTGATCCAGAGAAATGCTTCAACTACTACTACTACTACTACTACTACT 723  
QY 721 ACCTTTGCAAGAGGCTCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCT 780  
DB 724 ACCTTTGCAAGAGGCTCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCT 783  
QY 781 CATTTCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCT 840  
DB 784 CATTTCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCTCAAGGCTGCT 843  
QY 841 TGGGCTTGGAAAG 900  
DB 844 TGGGCTTGGAAAG 903  
QY 901 GATTCCTGCAAGAGGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 960  
DB 904 GATTCCTGCAAGAGGCTGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 963



QY 961 GCAGAAATGGGGGCTAGTGTATACAGATGAGGTTGAATTCAGAGATCTGCCATGC 1020  
DB 964 GCAGAAATGGGGGCTAGTGTATACAGATGAGGTTGAATTCAGAGATCTGCCATGC 1023  
QY 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCCCTGCTTGAAGTCCCAACCTCAACTT 1080  
DB 1024 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCCCTGCTTGAAGTCCCAACCTCAACTT 1083  
QY 1081 GAAACCCCATCTCTTAAAGCAGAGACTCAAGAGATCCCTTGTGCTTAACTGCGG 1140  
DB 1084 GAAACCCCATCTCTTAAAGCAGAGACTCAAGAGATCCCTTGTGCTTAACTGCGG 1143  
QY 1141 ACTCCATCCCAACCCATATCAATCCCACTGACCTGCTGTATCAAAAGACC 1200  
DB 1144 ACTCCATCCCAACCCATATCAATCCCACTGACCTGCTGTATCAAAAGACC 1203  
QY 1201 TCTCTGTGCTGAGTGTGCTTGTAGCTCACTGCTGCGGATGGAGAGAGACAGTGGC 1260  
DB 1204 TCTCTGTGCTGAGTGTGCTTGTAGCTCACTGCTGCGGATGGAGAGAGACAGTGGC 1263  
QY 1261 TTTTGTGGGCTATGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1320  
DB 1264 TTTTGTGGGCTATGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1323  
QY 1321 TGGAACTCCATCCCACTCTGTATGACCTCCAGAGTCCAGACTTATTTGTGACATGA 1380  
DB 1324 TGGAACTCCATCCCACTCTGTATGACCTCCAGAGTCCAGACTTATTTGTGACATGA 1383  
QY 1381 CTGAATTAACCACTCTTACGATATCCAGAGAAAGAGAACAGAGATGAGAGGA 1440  
DB 1384 CTGAATTAACCACTCTTACGATATCCAGAGAAAGAGAACAGAGATGAGAGGA 1443  
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472  
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

## RESULT 4

US-09-946-374-133  
Sequence 133, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
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PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
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PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
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PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
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PRIOR APPLICATION NUMBER: 60/100849  
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PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
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PRIOR APPLICATION NUMBER: 60/101071

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 PRIOR FILING DATE: 1998-10-08

PRIOR APPLICATION NUMBER: 60/103711  
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 PRIOR APPLICATION NUMBER: 60/105693  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105694  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 53.7%; Score 1472; DB 10; Length 1475;  
 Best Local Similarity 100.0%; Pred No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTAGAGTTCAAGGAGCAAG 60  
 DB 4 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTAGAGTTCAAGGAGCAAG 63  
 QY 61 GCTTCAGCTGGAAGCAAGGAGAGATCCCTGAAGACGCTTCTAATGAGGTTCCAT 120  
 DB 64 GCTTCAGCTGGAAGCAAGGAGAGATCCCTGAAGACGCTTCTAATGAGGTTCCAT 123  
 QY 121 GGCCTCTTGGGCTCAACTGTGGGCTAATCCTAGGCTTCTGGGCTTTTGGGCA 180  
 DB 124 GGCCTCTTGGGCTCAACTGTGGGCTAATCCTAGGCTTCTGGGCTTTTGGGCA 183  
 QY 181 ACTGTTGCGATGCTCTCCAGCTGGAACAACTTATGTCGTCAGCATTTGT 240  
 DB 184 ACTGTTGCGATGCTCTCCAGCTGGAACAACTTATGTCGTCAGCATTTGT 243  
 QY 241 GACAGCATGTTGCTTCTCCAGGCTCTGATGAGATGTCACACACAGCAAGCAT 300  
 DB 244 GACAGCATGTTGCTTCTCCAGGCTCTGATGAGATGTCACACACAGCAAGCAT 303  
 QY 301 CACCGATGATCATATAGCAACCTTCTGGGCTGCGCTGATCATCAGGCTGCCA 360  
 DB 304 CACCGATGATCATATAGCAACCTTCTGGGCTGCGCTGATCATCAGGCTGCCA 363  
 QY 361 GGCATGATGATGATCATGATGATGATGATGATGATGATGATGATGATGATG 420  
 DB 364 GGCATGATGATGATCATGATGATGATGATGATGATGATGATGATGATGATG 423  
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483  
 QY 481 TGGAGCTTTTATCTTGAAGGCTCGGAGATTCATTCGTTGCTGGAATCTTGA 540  
 DB 484 TGGAGCTTTTATCTTGAAGGCTCGGAGATTCATTCGTTGCTGGAATCTTGA 543  
 QY 541 TGGAGCTTACGGAATTCATCACTGATGATGATGATGATGATGATGATGATG 600  
 DB 544 TGGAGCTTACGGAATTCATCACTGATGATGATGATGATGATGATGATGATG 603  
 QY 601 AGAGGCTTTTACTTGGGATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 DB 604 AGAGGCTTTTACTTGGGATTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 663  
 QY 661 CTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 664 CTGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723



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PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101279
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PRIOR FILING DATE:	1998-09-23
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PRIOR FILING DATE:	1999-01-22

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3	PRIOR APPLICATION NUMBER: 60/119287	
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6	PRIOR FILING DATE: 1999-02-10	
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8	PRIOR FILING DATE: 1999-02-10	
9	PRIOR APPLICATION NUMBER: 60/120014	
10	PRIOR FILING DATE: 1999-02-11	
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12	PRIOR FILING DATE: 1999-04-13	
13	PRIOR APPLICATION NUMBER: 60/129674	
14	PRIOR FILING DATE: 1999-04-16	
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19	PRIOR APPLICATION NUMBER: 60/144791	
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21	PRIOR APPLICATION NUMBER: 60/169495	
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26	PRIOR FILING DATE: 2000-03-21	
27	PRIOR APPLICATION NUMBER: 60/199397	
28	PRIOR FILING DATE: 2000-04-25	
29	PRIOR APPLICATION NUMBER: 09/380139	
30	PRIOR FILING DATE: 1998-08-25	
31	PRIOR APPLICATION NUMBER: 09/311832	
32	PRIOR FILING DATE: 1999-05-14	
33	PRIOR APPLICATION NUMBER: 09/380137	
34	PRIOR FILING DATE: 1999-08-25	
35	PRIOR APPLICATION NUMBER: 09/380138	
36	PRIOR FILING DATE: 1999-08-25	
37	PRIOR APPLICATION NUMBER: 09/380142	

Query Match	53.7%	Score 1472	DB 13	Length 1475
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1472	0	Mismatches	0	Gaps 0

Oy	1	AGAAAGCAGCTGGGACGAGACCTCTGAAATGAGGGAATTAAAGGCTTCAAGACGACAGA	60
Dp	4	AGAAAGTCAGCTTGGCAGAGAGACCTCTGAATATGAGGGAATTAAAGGCTTCAAGACGACAGA	63
Oy	61	GCTTCAGCCTGAAGACAAAGGAGAGAGTCCCTGAGACGCTTCTATCTAGAGAGTTCGCAT	120
Dp	64	GCTTCAGCCTGAAGACAAAGGAGAGAGTCCCTGAGACGCTTCTATCTAGAGAGTTCGCAT	123
Oy	121	GGGCTCTCTGGGCTTCCAACTTGTGAGGCTTACATCTCTAGGCTTATGAGGCGCTTTTGGGCAC	180
Dp	124	GGGCTCTCTGGGCTTCCAACTTGTGAGGCTTACATCTCTAGGCTTATGAGGCGCTTTTGGGCAC	183
Oy	181	ACTGTGTGCATGTCTGCTCCCGACGTGAAAAACAAGTCTTATGTGCGTGGCACATTTGT	240
Dp	184	ACTGTGTGCATGTCTGCTCCCGACGTGAAAAACAAGTCTTATGTGCGTGGCACATTTGT	243
Oy	241	GACAGCAAGTTGGCTTCTCCAAAGGGCTCTGATATGAAATGTGTCACACACAGCACAGGCAT	300
Dp	244	GACAGCAAGTTGGCTTCTCCAAAGGGCTCTGATATGAAATGTGTCACACACAGCACAGGCAT	303
Oy	301	CACCCAGTGTACATCTATATAGCAACCTCTTGAGGCTTGCCGCTACATCCAGGCTGGCCA	360
Dp	304	CACCCAGTGTACATCTATATAGCAACCTCTTGAGGCTTGCCGCTACATCCAGGCTGGCCA	363
Oy	361	GGCCATGATGTGTACATCCAGTGCATCTCCTCCCTGAGCTGCATTAATCTCTGTGTGGG	420
Dp	364	GGCCATGATGTGTACATCCAGTGCATCTCCTCCCTGAGCTGCATTAATCTCTGTGTGGG	423
Oy	421	CATGAATATGCACAGCTTCTGTGCAGAGAAATCCCGAGCCAAAACACAGATGTGGCGTAAAGAG	480
Dp	424	CATGAATATGCACAGCTTCTGTGCAGAGAAATCCCGAGCCAAAACACAGATGTGGCGTAAAGAG	483

481 TGGAGCTTTTTCATCTTGGAGGCTCTGGAGTTCATTCTGTTGCTGGAATCTTCA 540  
484 TGGAGCTTTTTCATCTTGGAGGCTCTGGAGTTCATTCTGTTGCTGGAATCTTCA 543  
541 TGGAGCTTCAAGGACTTCTACTACCACTGTTGCTGAGAGATGAATTTGAGATTGG 600  
544 TGGAGCTTCAAGGACTTCTACTACCACTGTTGCTGAGAGATGAATTTGAGATTGG 603  
601 AGAGGCTTTTACTTGGGCAATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCTCT 660  
604 AGAGGCTTTTACTTGGGCAATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCTCT 663  
661 CTGCTTTTCTGCTCACTCCAGAGAAATGCTCCCACTAGATGCTTACCAAGGCCA 720  
664 CTGCTTTTCTGCTCACTCCAGAGAAATGCTCCCACTAGATGCTTACCAAGGCCA 723  
721 ACCTCTTGGCAAGAGCTCTCCAAAGGCTGTTCACTCCCAAGTCAAGAGTGT 780  
724 ACCTCTTGGCAAGAGGCTCTCCAAAGGCTGTTCACTCCCAAGTCAAGAGTGT 783  
781 CAATTCCTACAGCTTGAAGGCTTATGTGTAAGAACAGAGGCTGAGCTGGGGGCTGGC 840  
784 CAATTCCTACAGCTTGAAGGCTTATGTGTAAGAACAGAGGCTGAGCTGGGGGCTGGC 843  
841 TGGGCTGTGAAAGAAACAGTGAAGAGCAAGGAGGCTGAGAGGCTGAGAGGCTGAG 900  
844 TGGGCTGTGAAAGAAACAGTGAAGAGCAAGGAGGCTGAGAGGCTGAGAGGCTGAG 903  
901 GGAATCTGTCAAGAGGCTGCTGAGAGATGAGTGAATTTGGCATTGATGAGCAAG 960  
904 GGAATCTGTCAAGAGGCTGCTGAGAGATGAGTGAATTTGGCATTGATGAGCAAG 963  
961 GCGAATATGGGGGCTGATGTAAAGAGATGAGATGAGATGAGATGAGATGAGATGAG 1020  
964 GCGAATATGGGGGCTGATGTAAAGAGATGAGATGAGATGAGATGAGATGAGATGAG 1023  
1021 GAGCTTTTCTGTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
1024 GAGCTTTTCTGTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083  
1081 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGTGCTGCTGCTGCTGCTG 1140  
1084 GAAACCCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGTGCTGCTGCTGCTGCTG 1143  
1141 ACTCCATCCCAAAACCACTAATCACTCACTGACTGACTGACTGACTGACTGACTG 1200  
1144 ACTCCATCCCAAAACCACTAATCACTCACTGACTGACTGACTGACTGACTGACTG 1203  
1201 TCTCTCTGCTGAGTGTGCTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
1204 TCTCTCTGCTGAGTGTGCTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
1261 TTTTGTGGGCAATGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCT 1320  
1264 TTTTGTGGGCAATGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCT 1323  
1321 TGGAACTTCATCCCACTCTTGTGATGACTTCAAGTGTCAAGTGTCAAGTGTCAAG 1380  
1324 TGGAACTTCATCCCACTCTTGTGATGACTTCAAGTGTCAAGTGTCAAGTGTCAAG 1383  
1381 CTGAATTTAAACATCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCT 1440  
1384 CTGAATTTAAACATCTTAACTGCTTAACTGCTTAACTGCTTAACTGCTTAACTGCT 1443  
1441 CAGGAAGCAGCTTGGGCAATTTTAAATA 1472  
1444 CAGGAAGCAGCTTGGGCAATTTTAAATA 1475

RESULT 6  
US-10-063-547-79  
; Sequence 79, Application US/10063547

Publication No. US20020182638A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 79  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-547-79

Query Match 53.7%; Score 1472; DB 13; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGAAGTCAAGCTTGGCAGAGAGACTTGAATGAGGATTTAGAGTGTTCAGAGAGCAAGA 60  
4 AGAAGTCAAGCTTGGCAGAGAGACTTGAATGAGGATTTAGAGTGTTCAGAGAGCAAGA 63  
61 GCTTCAAGCTTGAAG 120  
64 GCTTCAAGCTTGAAG 123  
121 GGCCTCTTGTGCTTCACTTGTGAGGCTTCACTAGGCTTCTGAGGCTTTTGGGCAAC 180  
124 GGCCTCTTGTGCTTCACTTGTGAGGCTTCACTAGGCTTCTGAGGCTTTTGGGCAAC 183  
181 ACTGTTGCTGAGTGTGCTTCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
184 ACTGTTGCTGAGTGTGCTTCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
241 GAGAGAGTGTGCTTCTTCAAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
244 GAGAGAGTGTGCTTCTTCAAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303  
301 CACCAAGTGAATCTATAGCACTTCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 360  
304 CACCAAGTGAATCTATAGCACTTCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 363  
361 GGCATGATGATGATCACTCAAGTCAATCTTCTGAGGCTGAGAGAGAGAGAGAGAGAG 420  
364 GGCATGATGATGATCACTCAAGTCAATCTTCTGAGGCTGAGAGAGAGAGAGAGAGAG 423  
421 CATGAGATGACAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
424 CATGAGATGACAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483  
481 TGAAGCTTTTTCATCTTGAAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
484 TGAAGCTTTTTCATCTTGAAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543  
541 TGGAGTCTTCAAGGACTTCTACTACCACTGTTGCTGAGAGATGAATTTGAGATTGG 600  
544 TGGAGTCTTCAAGGACTTCTACTACCACTGTTGCTGAGAGATGAATTTGAGATTGG 603  
601 AGAGGCTTTTACTTGGGCAATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCTCT 660  
604 AGAGGCTTTTACTTGGGCAATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCTCT 663  
661 CTGCTTTTCTGCTCACTCCAGAGAAATGCTCCCACTAGATGCTTACCAAGGCCA 720

Db	664	CTGCTTTTCTGCTCATCCCAAGAAATGGCTTCAACTACTACGATGCTTACCAAGCCCA	723
Qy	721	ACCTCTTGCCACAGAGCTCTTCCAAAGCCTGCTCAACCTCCCAAGTCAAGAGTGT	780
Db	724	ACCTCTTGCCACAGAGCTCTTCCAAAGCCTGCTCAACCTCCCAAGTCAAGAGTGT	783
Qy	781	CAATTCTTCAAGCTTCAAGGGGTATGTGTGAGAAACCAAGGGGCAAGAGCTGGGGGGTGC	840
Db	784	CAATTCTTCAAGCTTCAAGGGGTATGTGTGAGAAACCAAGGGGCAAGAGCTGGGGGGTGC	843
Qy	841	TGGGTCTGTGAAAAACAGTGAAGCAGCAACCCCGAGGGGCAAGGTGAGGGCACTACCACT	900
Db	844	TGGGTCTGTGAAAAACAGTGAAGCAGCAACCCCGAGGGGCAAGGTGAGGGCACTACCACT	903
Qy	901	GGATCGTGCAGAGGTGCTGCTGAGATGACTGACTTTGGCCATTGGAATTGAGCAAG	960
Db	904	GGATCGTGCAGAGGTGCTGCTGAGATGACTGACTTTGGCCATTGGAATTGAGCAAG	963
Qy	961	GCAGAAATGGGGGGCTTAGTGTAAACAGATGCAAGTTGAATTGCCAAGATGCTGCCATGC	1020
Db	964	GCAGAAATGGGGGGCTTAGTGTAAACAGATGCAAGTTGAATTGCCAAGATGCTGCCATGC	1020
Qy	1021	CAGCCTTCTGTCTTCTGCTGACCTGCTGCTCCCTGCGCCCTGAATGCCCAACCTCAACTT	1080
Db	1024	CAGCCTTCTGTCTTCTGCTGACCTGCTGCTCCCTGCGCCCTGAATGCCCAACCTCAACTT	1080
Qy	1081	GAAACCCCATTCCTCTTAAGCCAGAGACTCAGAGATCCCTTGGCCTGTGTTTAACTGGG	1144
Db	1084	GAAACCCCATTCCTCTTAAGCCAGAGACTCAGAGATCCCTTGGCCTGTGTTTAACTGGG	1144
Qy	1141	ACTCCATCCCAAAACCCCAATATCAGATCCCACTGAAGCTGCTGTGTCAAAAGCCC	1200
Db	1144	ACTCCATCCCAAAACCCCAATATCAGATCCCACTGAAGCTGCTGTGTCAAAAGCCC	1200
Qy	1201	TCTCTCTGGCTAGAGTGGGCTGTAGCTATGCTGAGGGGATGGGAAAGAGAACAGTGGC	1266
Db	1204	TCTCTCTGGCTAGAGTGGGCTGTAGCTATGCTGAGGGGATGGGAAAGAGAACAGTGGC	1266
Qy	1261	TTTTGTGGGCAATGTGCTTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC	1322
Db	1264	TTTTGTGGGCAATGTGCTTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC	1322
Qy	1321	TGAAACCTTCATCCACTCTTGTATGACTCCAGATGCTCAGACTAATTTGTGCATGA	1380
Db	1324	TGAAACCTTCATCCACTCTTGTATGACTCCAGATGCTCAGACTAATTTGTGCATGA	1380
Qy	1381	CTGAATTAATAACCATTCCTACGGGTATTCAGAGGAAACAAAGACAGATGCAAGATGGAGGA	1444
Db	1384	CTGAATTAATAACCATTCCTACGGGTATTCAGAGGAAACAAAGACAGATGCAAGATGGAGGA	1444
Qy	1441	CAGGAAGCAGCCTGGGACATTTAAAAAATA	1472
Db	1444	CAGGAAGCAGCCTGGGACATTTAAAAAATA	1475
RESULT 7			
US-10-063-551-79			
: Sequence 79, Application US/10063551			
: Publication No. US20020183494A1			
GENERAL INFORMATION:			
: APPLICANT: Eaton, Dan L.			
: APPLICANT: Filvaroff, Ellen			
: APPLICANT: Geritsen, Mary E.			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Goddard, Paul J.			
: APPLICANT: Grimaldi, Christopher J.			
: APPLICANT: Gurney, Austin L.			
: APPLICANT: Watanabe, Colin K.			
: APPLICANT: Wood, William I.			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
: FILE REFERENCE: P3230R1C1			

[illegible]



QY 901 GGATCGTGCAGAGGNGCTGTAGAGTAGACTTTGGCCATTGATGAGCAAG 960  
DB 904 GGATCGTGCAGAGGNGCTGTAGAGTAGACTTTGGCCATTGATGAGCAAG 963  
QY 961 GCAGAAATGGGGCTAGTGTATACAGATGAGGTTGATTCAGAGATGCTGCCATGC 1020  
DB 964 GCAGAAATGGGGCTAGTGTATACAGATGAGGTTGATTCAGAGATGCTGCCATGC 1023  
QY 1021 CAGCCTTTCTGTTTCTTCTCACTTGTCTGCTCCCTGCTTAACTTCCCACTT 1080  
DB 1024 CAGCCTTTCTGTTTCTTCTCACTTGTCTGCTCCCTGCTTAACTTCCCACTT 1083  
QY 1081 GAAACCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCCTGTTTACCTGGG 1140  
DB 1084 GAAACCCATTCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCCTGTTTACCTGGG 1143  
QY 1141 ACTCCATCCCAACCCACTATCATCTCCACTGATGACCTCTGTGTATCAAGACCC 1200  
DB 1144 ACTCCATCCCAACCCACTATCATCTCCACTGATGACCTCTGTGTATCAAGACCC 1203  
QY 1201 TCTCTCTGCTGAGTGGTCTTTAGCTCATTTGCTGGGATGGGAGAGAGACAGTGGC 1260  
DB 1204 TCTCTCTGCTGAGTGGTCTTTAGCTCATTTGCTGGGATGGGAGAGACAGTGGC 1263  
QY 1261 TTTTGGGGATGCTCTAAGCTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1320  
DB 1264 TTTTGGGGATGCTCTAAGCTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1323  
QY 1321 TGGAACTCCATCCCACTTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1380  
DB 1324 TGGAACTCCATCCCACTTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1383  
QY 1381 CTGAAATTAACCATCTCTAGTATCCAGGAAACAGAAACAGAGATGAGAGGA 1440  
DB 1384 CTGAAATTAACCATCTCTAGTATCCAGGAAACAGAAACAGAGATGAGAGGA 1443  
QY 1441 CAGGAAGGAGCCTTGGAGCATTTAAAAATA 1472  
DB 1444 CAGGAAGGAGCCTTGGAGCATTTAAAAATA 1475

RESULT 8  
US-10-028-072-491  
Sequence 491, Application US/10028072  
Publication No. US2003004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028, 072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
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PRIOR FILING DATE: 1997-09-24  
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PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
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PRIOR FILING DATE: 1997-10-29  
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PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: 60/069694  
 PRIOR FILING DATE: 1997-12-16  
 PRIOR APPLICATION NUMBER: 60/072320  
 PRIOR FILING DATE: 1998-01-23  
 PRIOR APPLICATION NUMBER: 60/073612  
 PRIOR FILING DATE: 1998-02-04  
 PRIOR APPLICATION NUMBER: 60/074086  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/074092  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/077791  
 PRIOR FILING DATE: 1998-03-12  
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 PRIOR APPLICATION NUMBER: 60/081818  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082999  
 PRIOR FILING DATE: 1998-04-24  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084637  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085149  
 PRIOR FILING DATE: 1998-05-12  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
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 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/086414  
 PRIOR FILING DATE: 1998-05-22  
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 PRIOR FILING DATE: 1998-05-22  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/088026  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088730  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088741  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088810  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088858

PRIOR FILING DATE: 19/98-06-11  
 PRIOR APPLICATION NUMBER: 60/089532  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089599  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089947  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/090349  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090538  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090663  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGGTCTTCAAGAGCAAA 60  
 DB 4 AGAAGTCAGCTGGCAGAGAGACTGGAATGAGGATTTAGAGGTCTTCAAGAGCAAA 63  
 QY 61 GCTTCAGCTGGAAGCAAGGAGAGAGCTCCCTGGAAGCGCTTCTACTGAGAGGTCTGCAT 120  
 DB 64 GCTTCAGCTGGAAGCAAGGAGAGAGCTCCCTGGAAGCGCTTCTACTGAGAGGTCTGCAT 123  
 QY 121 GGCCTCTCTTGGCTCCCACTTGTGGGCTTACATCTAGAGCTTCTGGGCTTTTGGGCA 180  
 DB 124 GGCCTCTCTTGGCTCCCACTTGTGGGCTTACATCTAGAGCTTCTGGGCTTTTGGGCA 183  
 QY 181 ACTGGTTGCATGCTGCTCTCCCAAGCTGGAAGCAAGTTCTTATGTGGTCCAGCATTT 240  
 DB 184 ACTGGTTGCATGCTGCTCTCCCAAGCTGGAAGCAAGTTCTTATGTGGTCCAGCATTT 243  
 QY 241 GACAGAGTTGGCTTCCAGAGGCTCTGAGTGAATGTGCAACACAGCAAGGCAAT 300  
 DB 244 GACAGAGTTGGCTTCCAGAGGCTCTGAGTGAATGTGCAACACAGCAAGGCAAT 303  
 QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTTGCCTGACATCCAGGCTGCCA 360  
 DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTTGCCTGACATCCAGGCTGCCA 363  
 QY 361 GGCATGATGTGACATCTGCAATCTCTTCCTGAGCTGATATCTCTGTGTGG 420  
 DB 364 GGCATGATGTGACATCTGCAATCTCTTCCTGAGCTGATATCTCTGTGTGG 423  
 QY 421 CATGAGATGACAGTCTTTCGCAAGGATCCGAGCAAGACAGAGTGGCGGTAGCAG 480  
 DB 424 CATGAGATGACAGTCTTTCGCAAGGATCCGAGCAAGACAGAGTGGCGGTAGCAG 483  
 QY 481 TGAAGTCTTTTATCTCTTGAAGGCTCTCTGGAGATTCATCTCTGTGCTTGAATCTTCA 540  
 DB 484 TGAAGTCTTTTATCTCTTGAAGGCTCTCTGGAGATTCATCTCTGTGCTTGAATCTTCA 543  
 QY 541 TGGGATCTTGAAGGATTTTACTCACCACTGTGCTGACAGATGAATTTGAGATTGG 600  
 DB 544 TGGGATCTTGAAGGATTTTACTCACCACTGTGCTGACAGATGAATTTGAGATTGG 603  
 QY 601 AGAGGCTCTTGAAGGATTTTCTTCCCTGTTTCCCGATGAGAGGATATCTCT 660  
 DB 604 AGAGGCTCTTGAAGGATTTTCTTCCCTGTTTCCCGATGAGAGGATATCTCT 663

QY 661 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 720  
Db 664 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTACTAGATGCTTACCAAGCCCA 723  
QY 721 ACCTTTTGCCAGAGAGCTCTCCAGAGCTGCTCAACCTTCCCAAGTCAAGTGAAT 780  
Db 724 ACCTTTTGCCAGAGAGCTCTCCAGAGCTGCTCAACCTTCCCAAGTCAAGTGAAT 783  
QY 781 CAATTCTTCAAGCTGACAGGATATGTGTGAAGAACAGAGGGGCTGAGGGGGTGGC 840  
Db 784 CAATTCTTCAAGCTGACAGGATATGTGTGAAGAACAGAGGGGCTGAGGGGGTGGC 843  
QY 841 TGGGCTGTGAAAAACAGTGAAGAGACCCGAGAGGGCCAGAGTGAAGGACACTACCACT 900  
Db 844 TGGGCTGTGAAAAACAGTGAAGAGACCCGAGAGGGCCAGAGTGAAGGACACTACCACT 903  
QY 901 GATTCGTGACAGAGGTGCTGAGAGATGACTGACTTTTGCCATTGGAATTGACCAAG 960  
Db 904 GATTCGTGACAGAGGTGCTGAGAGATGACTGACTTTTGCCATTGGAATTGACCAAG 963  
QY 961 GCGAATATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATGCTGCCATGC 1020  
Db 964 GCGAATATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATGCTGCCATGC 1023  
QY 1021 CAGGCTTTCTGTTTCTCTCACTTGTGCTGCCCTGCCCTTAAGTCCCAACCTCACTT 1080  
Db 1024 CAGGCTTTCTGTTTCTCTCACTTGTGCTGCCCTGCCCTTAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGCTGTTTAACTGAG 1140  
Db 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTTGCTGCTGTTTAACTGAG 1143  
QY 1141 ACTTCATCCCAAAACCACTAATATCATCCCATGACCTCTGTGATCAAAAGCCC 1200  
Db 1144 ACTTCATCCCAAAACCACTAATATCATCCCATGACCTCTGTGATCAAAAGCCC 1203  
QY 1201 TCTCTGCTGAGTGGTGGCTTGAAGCTCAATGCTGAGGAAATGGGAAAGAGAGAGTGGC 1260  
Db 1204 TCTCTGCTGAGTGGTGGCTTGAAGCTCAATGCTGAGGAAATGGGAAAGAGAGAGTGGC 1263  
QY 1261 TTTTGTGGGATTTGCTTAACTTAATCTCAAGCTTCCCTCAAAAGAACTGATTTGGCCC 1320  
Db 1264 TTTTGTGGGATTTGCTTAACTTAATCTCAAGCTTCCCTCAAAAGAACTGATTTGGCCC 1323  
QY 1321 TGGAACTCCATCCCACTCTTTGTATATGATCTCAGAGTGTCCAGACTAATTTTGTGATGAA 1380  
Db 1324 TGGAACTCCATCCCACTCTTTGTATATGATCTCAGAGTGTCCAGACTAATTTTGTGATGAA 1383  
QY 1381 CTGAATTAATAACAATCTTAAGGATATCAAGGAAACAGAAAGAGAGATGAGAGAGGA 1440  
Db 1384 CTGAATTAATAACAATCTTAAGGATATCAAGGAAACAGAAAGAGAGATGAGAGAGGA 1443  
QY 1441 CAGGAAGCAGCTGAGCAATTTAAAAAATA 1472  
Db 1444 CAGGAAGCAGCTGAGCAATTTAAAAAATA 1475

## RESULT 9

US-10-063-616-79  
; Sequence 79, Application US/10063616  
; Publication No. US20030013855A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Geritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,616  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 79  
; LENGTH: 1475  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-616-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTTGGCAGAGAGACTTGAATATGAGGATTTAGAGTGTTCAGAGAGCAAGA 60  
Db 4 AGAAGTCAGCTTGGCAGAGAGACTTGAATATGAGGATTTAGAGTGTTCAGAGAGCAAGA 63  
QY 61 GCTTCAGGCTGAAAGACAAAGGAGACAGTCCCTGAAGACGCTTCTAAGAGAGTCTGACAT 120  
Db 64 GCTTCAGGCTGAAAGACAAAGGAGACAGTCCCTGAAGACGCTTCTAAGAGAGTCTGACAT 123  
QY 121 GGCCTCTCTTGGGCTCCCACTTGTGGGCTAATCTAGAGCTTCTGAGGCTTTTGGGAC 180  
Db 124 GGCCTCTCTTGGGCTCCCACTTGTGGGCTAATCTAGAGCTTCTGAGGCTTTTGGGAC 183  
QY 181 ACTGTTTGCATGCTGCTCCCACTGAGAAACAAAGTTCTTAATGTGCTGCTCAGCATTT 240  
Db 184 ACTGTTTGCATGCTGCTCCCACTGAGAAACAAAGTTCTTAATGTGCTGCTCAGCATTT 243  
QY 241 GACAGAGTGGCTTCTCCCAAGGGGCTCTGAGATGAGATGAGCAACACAGACAGGACAT 300  
Db 244 GACAGAGTGGCTTCTCCCAAGGGGCTCTGAGATGAGATGAGCAACACAGACAGGACAT 303  
QY 301 CACCAAGTGTGACATCTAATAGCAACCTTCTGAGGCTGCCCCGCTGACATCCAGGCTGCCA 360  
Db 304 CACCAAGTGTGACATCTAATAGCAACCTTCTGAGGCTGCCCCGCTGACATCCAGGCTGCCA 363  
QY 361 GGCATGATGTGACATCCAGTGCATCTCTCTGCTGCTGCTGATTAATCTGTGTGGG 420  
Db 364 GGCATGATGTGACATCCAGTGCATCTCTCTGCTGCTGCTGATTAATCTGTGTGGG 423  
QY 421 CATGAGATGACAGTCTTCTGCAAGAAATCCGAGGCCAAGACAGATGAGGAGGAGG 480  
Db 424 CATGAGATGACAGTCTTCTGCAAGAAATCCGAGGCCAAGACAGATGAGGAGGAGG 483  
QY 481 TGAAGTCTTTTCAATCCTTGAAGGCTCTGAGATTCATCTGTGCTGGAATCTTCA 540  
Db 484 TGAAGTCTTTTCAATCCTTGAAGGCTCTGAGATTCATCTGTGCTGGAATCTTCA 543  
QY 541 TGGGATCTTACGAGGACTTCTAATCAACATGAGTGTCTGACAGATGAATTTGAATTGG 600  
Db 544 TGGGATCTTACGAGGACTTCTAATCAACATGAGTGTCTGACAGATGAATTTGAATTGG 603  
QY 601 AGAGGCTCTTAACTTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 660  
Db 604 AGAGGCTCTTAACTTGGGCAATTAATTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 663  
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCCAACTAAGATGAGTGAATTTGAAGTGAAT 720  
Db 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTCCAACTAAGATGAGTGAATTTGAAGTGAAT 723  
QY 721 ACCTTTTGCCAGAGAGCTCTCCAGAGCTGCTCAACCTTCCCAAGTCAAGTGAAT 780  
Db 724 ACCTTTTGCCAGAGAGCTCTCCAGAGCTGCTCAACCTTCCCAAGTCAAGTGAAT 783  
QY 781 CAATTCTTCAAGCTGACAGGATATGTGTGAAGAACAGAGGGGCTGAGGGGGTGGC 840  
Db 784 CAATTCTTCAAGCTGACAGGATATGTGTGAAGAACAGAGGGGCTGAGGGGGTGGC 843  
QY 841 TGGGCTGTGAAAAACAGTGAAGAGACCCGAGAGGGCCAGAGTGAAGGACACTACCACT 900

Db	844	TGGGCTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTAGAGGACACTACACT	903
Qy	901	GGATCGTGTCAAGAGGTCTGTGAGATAGA CTAGCTTTTGCCATTGGATTGAGCAAG	960
Db	904	GGATCGTGTCAAGAGGTCTGTGAGATAGA CTAGCTTTTGCCATTGGATTGAGCAAG	963
Qy	961	GCAGAAATGGGGGGCTAGGTGTAA CAGCATGTCAAGTGTGAATTGGCAAGATGCTGGCATGC	1022
Db	964	GCAGAAATGGGGGGCTAGGTGTAA CAGCATGTCAAGTGTGAATTGGCAAGATGCTGGCATGC	1023
Qy	1021	CAGCCTTCTGTGTTTCTCTACCTGTCTGCTCCGCTGAGTCCCAAGCCCTCAACTT	1086
Db	1024	CAGCCTTCTGTGTTTCTCTACCTGTCTGCTCCGCTGAGTCCCAAGCCCTCAACTT	1087
Qy	1081	GAAACCCCATTTCCCTTAAAGCAGAGCTCAGAGGATCCCTTGGCCCTGTGTTTACCTGGG	1140
Db	1084	GAAACCCCATTTCCCTTAAAGCAGAGCTCAGAGGATCCCTTGGCCCTGTGTTTACCTGGG	1143
Qy	1141	ACTGCATCTCCCAAAACCCACTATATCA CACTCCCACTGACTGACCTCTGTGTATTAAGACCC	1200
Db	1144	ACTGCATCTCCCAAAACCCACTATATCA CACTCCCACTGACTGACCTCTGTGTATTAAGACCC	1203
Qy	1201	TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTTGCTGGGGATGGGAAAGGAGACGTTGGC	1266
Db	1204	TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTTGCTGGGGATGGGAAAGGAGACGTTGGC	1269
Qy	1261	TTTTGTGGGCAATTGCTCTTACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC	1320
Db	1264	TTTTGTGGGCAATTGCTCTTACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC	1323
Qy	1321	TGGAACCTTCATCCCACTCTGTTTATGACTCACA CAGTGTCCAAGCTAATTGTGTGATGA	1380
Db	1324	TGGAACCTTCATCCCACTCTGTTTATGACTCACA CAGTGTCCAAGCTAATTGTGTGATGA	1383
Qy	1381	CTGAATATTAACCATCTTACGGTATCCAGGGGAA CAGAAAGCAGATGTGAGGATGGGAGGA	1440
Db	1384	CTGAATATTAACCATCTTACGGTATCCAGGGGAA CAGAAAGCAGATGTGAGGATGGGAGGA	1443
Qy	1441	CAGGAAGCAGACCTGGGACATTTAAAAAAATA	1472
Db	1444	CAGGAAGCAGACCTGGGACATTTAAAAAAATA	1475
RESULT 10			
US-10-140-808-491			
: Sequence 491, Application US/10140808			
: Publication No. US20030017563A1			
GENERAL INFORMATION:			
: APPLICANT: Baker, Kevin P.			
: APPLICANT: Beresini, Maureen			
: APPLICANT: Deforge, Laura			
: APPLICANT: Filvaroff, Ellen			
: APPLICANT: Gao, Wei-Qiang			
: APPLICANT: Gerritsen, Mary E.			
: APPLICANT: Goddard, Audrey			
: APPLICANT: Godowski, Paul J.			
: APPLICANT: Gurney, Austin L.			
: APPLICANT: Sherwood, Steven			
: APPLICANT: Smith, Victoria			
: APPLICANT: Stewart, Timothy A.			
: APPLICANT: Tumas, Daniel			
: APPLICANT: Watanabe, Colin K			
: APPLICANT: Wood, William			
: APPLICANT: Zhang, Zemin			
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
: TITLE OF INVENTION: ACIDS ENCODING THE SAME			
: FILE REFERENCE: P3303R1C182			
: CURRENT APPLICATION NUMBER: US/10/140,808			
: CURRENT FILING DATE: 2002-05-07			
: Prior Application removed - See File Wrapper or Palm			
: NUMBER OF SEQ ID NOS: 550			

Query Match	53.7%	Score 1472;	DB 14;	Length 1475;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1472;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
;	SEO_ID NO 491			
;	LENGTH: 1475			
;	TYPE: DNA			
;	ORGANISM: Homo Sapien			
US-10-140-808-491				
QY	1	AGAAATCAGCCTGGCAGAGAGACTCTGAAATAGAGGATTTAGAGGTGTTCAAGAGACAGA	60	
DB	4	AGAAGTACGCTGGAGAGAGACTCTGAAATAGAGGATTTAGAGGTGTTCAAGAGACAGA	63	
QY	61	GCTTCAGCTGAAAGCAAGGGAGCAGTCCCTGAAAGCGCTTCTACTGAGAGGTCTGCAT	120	
DB	64	GCTTCAGCTGAAAGCAAGGGAGCAGTCCCTGAAAGCGCTTCTACTGAGAGGTCTGCAT	123	
QY	121	GGCCCTCTTGGCCCTCCAACTTTGGGGTTAATCCTAGGCCCTTCTGGGGCTTTGGGGAC	180	
DB	124	GGCCCTCTTGGCCCTCCAACTTTGGGGTTAATCCTAGGCCCTTCTGGGGCTTTGGGGAC	183	
QY	181	ACTGGTTGCATGCTGCTCCCCAGCTGGAAAAAAGATTCTTATGCGGTGCAGCATTTG	240	
DB	184	ACTGGTTGCATGCTGCTCCCCAGCTGGAAAAAAGATTCTTATGCGGTGCAGCATTTG	243	
QY	241	GACAGCAGTTGGCTTCTTCCAAAGGGCTCTGAGTGAATGTGCCACACACAGCACAGGCAT	300	
DB	244	GACAGCAGTTGGCTTCTTCCAAAGGGCTCTGAGTGAATGTGCCACACACAGGCAT	303	
QY	301	CACCCAGTGTACATCTATACACCCCTTGGGGCTGGCCGCTGACATTCAGAGGCTGCCCA	360	
DB	304	CACCCAGTGTACATCTATACACCCCTTGGGGCTGGCCGCTGACATTCAGAGGCTGCCCA	363	
QY	361	GGCCATGATGTGTGACATCCAGTGCAGATCTCTCCCTGGCTGCAATTATCTCTGTGGGG	420	
DB	364	GGCCATGATGTGTGACATCCAGTGCAGATCTCTCCCTGGCTGCAATTATCTCTGTGGGG	423	
QY	421	CATAGATGACACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	480	
DB	424	CATAGATGACACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	483	
QY	481	TGGAGTCTTTTCAATCCTTGGAGGCTCTCTGGGATTCATTCTGTGTGCTTGGAAATCTTCA	540	
DB	484	TGGAGTCTTTTCAATCCTTGGAGGCTCTCTGGGATTCATTCTGTGTGCTTGGAAATCTTCA	543	
QY	541	TGGATTCCTACGGGACTTCTACACACATGGTGCCTGACAGCATGAAATTTGAGATTGG	600	
DB	544	TGGATTCCTACGGGACTTCTACACACATGGTGCCTGACAGCATGAAATTTGAGATTGG	603	
QY	601	AGAGGCTCTTACTTGGGCAATTATTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCTT	660	
DB	604	AGAGGCTCTTACTTGGGCAATTATTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCTT	663	
QY	661	CTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCCACTATCTACATGATGCTTACCAAGCCCA	720	
DB	664	CTGCTTTTCTGCTCATCTCCAGAGAAATCGCTCCACTATCTACATGATGCTTACCAAGCCCA	723	
QY	721	ACCTCTTGGCAAGAGAGCTCTCCAGGGCCGTGTCAACCTCCCAAAGTCAAGAGTAGTT	780	
DB	724	ACCTCTTGGCAAGAGAGCTCTCCAGGGCCGTGTCAACCTCCCAAAGTCAAGAGTAGTT	783	
QY	781	CAATTCTCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCCAGAGACTGGGGGGTGGC	840	
DB	784	CAATTCTCTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCCAGAGACTGGGGGGTGGC	843	
QY	841	TGGGTTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGTGAAGGACATTAACAAT	900	
DB	844	TGGGTTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGTGAAGGACATTAACAAT	903	
QY	901	GGATTCGTGTCAAGAGGTGTGCTGTAGAGATAGACTGATCTTTGGCCATTGGATTGGCAAG	960	
DB	904	GGATTCGTGTCAAGAGGTGTGCTGTAGAGATAGACTGATCTTTGGCCATTGGATTGGCAAG	963	

QY 961 GCAGAAATGGGGGCTAGTGTATGAGATGAGAGTGAATTGCCAAGGATGCTGCCATGC 1020  
DB 964 GCAGAAATGGGGGCTAGTGTATGAGATGAGAGTGAATTGCCAAGGATGCTGCCATGC 1023  
QY 1021 CAGCCTTTCTGTTTCTCTCACTTGTCTGCCCTGCTTGAAGTCCCAACCTCACTT 1080  
DB 1024 CAGCCTTTCTGTTTCTCTCACTTGTCTGCCCTGCTTGAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTGAGAGATCCCTTGGCTTGTGTTAACTGGG 1140  
DB 1084 GAAACCCCATTTCCCTTAAGCAGAGACTGAGAGATCCCTTGGCTTGTGTTAACTGGG 1143  
QY 1141 ACTCCATCCCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1200  
DB 1144 ACTCCATCCCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1203  
QY 1201 TCTCTGTGCTGAGTGTGCTCTTGTATGATCCAGATGTCAGACTAATTTGTGCAATGA 1260  
DB 1204 TCTCTGTGCTGAGTGTGCTCTTGTATGATCCAGATGTCAGACTAATTTGTGCAATGA 1263  
QY 1261 TTTTGTGGGCTATGCTCTTAACCTAATCTCAAGCTTCCCTCAAGAACTGATGGCCC 1320  
DB 1264 TTTTGTGGGCTATGCTCTTAACCTAATCTCAAGCTTCCCTCAAGAACTGATGGCCC 1323  
QY 1321 TGGACCTCCATCCCACTCTTGTATGATCCAGATGTCAGACTAATTTGTGCAATGA 1380  
DB 1324 TGGACCTCCATCCCACTCTTGTATGATCCAGATGTCAGACTAATTTGTGCAATGA 1383  
QY 1381 CTGAATTAATAACCATCTCAAGGATATCCAGAGAAAGAGAACAGAGATGAGAGGA 1440  
DB 1384 CTGAATTAATAACCATCTCAAGGATATCCAGAGAAAGAGAACAGAGATGAGAGGA 1443  
QY 1441 CAGGAAGGAGGCTGGGACATTTAAAAATA 1472  
DB 1444 CAGGAAGGAGGCTGGGACATTTAAAAATA 1475

RESULT 11  
US-10-063-569-79  
Sequence 79, Application US/10063569  
Publication No. US20030018168A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Pilleroff, Ellen  
APPLICANT: Gerilsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,569  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 79  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-569-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGACTCTGAATGAGAGTTAGAGGTGTTCAAGAGCAAGA 60  
DB 4 AGAAGTCAGCTGGCAGAGACTCTGAATGAGAGTTAGAGGTGTTCAAGAGCAAGA 63

QY 61 GCTTCAGCCTGAAGACAGAGGAGCACTCCCTGAGACGCTTCTAATGAGAGTCTGCCAT 120  
DB 64 GCTTCAGCCTGAAGACAGAGGAGCACTCCCTGAGACGCTTCTAATGAGAGTCTGCCAT 123  
QY 121 GGCCTCTCTTGGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGCAC 180  
DB 124 GGCCTCTCTTGGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGCAC 183  
QY 181 ACTGTTGGCAGTCTGCTGCCAGCTGGAAGAAAGAGTCTTATGTGGGTGCCAGATTTGT 240  
DB 184 ACTGTTGGCAGTCTGCTGCCAGCTGGAAGAAAGAGTCTTATGTGGGTGCCAGATTTGT 243  
QY 241 GACAGAGTTGGGCTTCTCAAGGAGCCTCTGATGAAATGTGCCACACAGACAGGCAAT 300  
DB 244 GACAGAGTTGGGCTTCTCAAGGAGCCTCTGATGAAATGTGCCACACAGACAGGCAAT 303  
QY 301 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCA 360  
DB 304 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTGCCA 363  
QY 361 GGCAGATGAGTGAATCCAGATGCAATCTCCCTGGGCTGCAATATCTGTGGTGGG 420  
DB 364 GGCAGATGAGTGAATCCAGATGCAATCTCCCTGGGCTGCAATATCTGTGGTGGG 423  
QY 421 CATGAGATGACAGTCTTCTGCAAGAAATCCAGAGCAAGAGAGAGTGGCGGTAGCAGG 480  
DB 424 CATGAGATGACAGTCTTCTGCAAGAAATCCAGAGCAAGAGAGTGGCGGTAGCAGG 483  
QY 481 TGAAGTCTTTTCACTCTTGAAGGCTCTGGGATTCATCTGTGCTCTGAAATCTTCA 540  
DB 484 TGAAGTCTTTTCACTCTTGAAGGCTCTGGGATTCATCTGTGCTCTGAAATCTTCA 543  
QY 541 TGGGATTCAGAGGAGCTTCTCACTCAAGCTGAGCTGAGAGATGAAATTTGAGATTGG 600  
DB 544 TGGGATTCAGAGGAGCTTCTCACTCAAGCTGAGCTGAGAGATGAAATTTGAGATTGG 603  
QY 601 AGAGGCTCTTACTTGGGCAATTTCTTCCCTGTCTCCCTGATAGCTGGAATCAATCT 660  
DB 604 AGAGGCTCTTACTTGGGCAATTTCTTCCCTGTCTCCCTGATAGCTGGAATCAATCT 663  
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGGCTCCAACTACTAGATGCTTACCAAGCCCA 720  
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGGCTCCAACTACTAGATGCTTACCAAGCCCA 723  
QY 721 ACCTTTGGCAGAGAGCTCTCAAGGCTGCTGTCAACTCCCAAGTCAAGAGTGAAT 780  
DB 724 ACCTTTGGCAGAGAGCTCTCAAGGCTGCTGTCAACTCCCAAGTCAAGAGTGAAT 783  
QY 781 CAATTCCTACAGCTGACAGGATGATGTGAAGAAACAGAGGAGCAGAGCTGAGGAGTGGC 840  
DB 784 CAATTCCTACAGCTGACAGGATGATGTGAAGAAACAGAGGAGCAGAGCTGAGGAGTGGC 843  
QY 841 TGGGCTGTGAAAGAGTGAAGACAGCAGGAGGAGCAGAGTGAAGGAGCACTACCACT 900  
DB 844 TGGGCTGTGAAAGAGTGAAGAGCAGCAGGAGGAGCAGAGTGAAGGAGCACTACCACT 903  
QY 901 GGAATCGTGAAGAGTGTGCTGAGAGTGAATGACTTTGGGCAATTTGAGTGAAGCAAG 960  
DB 904 GGAATCGTGAAGAGTGTGCTGAGAGTGAATGACTTTGGGCAATTTGAGTGAAGCAAG 963  
QY 961 GCAGAAATGGGGGCTAGTGTATGAGATGAGAGTGAATTGCCAAGGATGCTGCCATGC 1020  
DB 964 GCAGAAATGGGGGCTAGTGTATGAGATGAGAGTGAATTGCCAAGGATGCTGCCATGC 1023  
QY 1021 CAGCCTTTCTGTTTCTCTCACTTGTCTGCCCTGCTTGAAGTCCCAACCTCACTT 1080  
DB 1024 CAGCCTTTCTGTTTCTCTCACTTGTCTGCCCTGCTTGAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTGAGAGATCCCTTGGCTTGTGTTAACTGGG 1140  
DB 1084 GAAACCCCATTTCCCTTAAGCAGAGACTGAGAGATCCCTTGGCTTGTGTTAACTGGG 1143  
QY 1141 ACTCCATCCCCCAACCACTAATCAATCCCACTGATGACCTCTGTATCAAGACCC 1200

DB 1144 ACTCCATCCCAAAACCAATCAATCCACATGACCTCTGTGTCAAAAGCCC 1203  
QY 1201 TCTCTGCTGAGTGTGCTCTTAGCTCATTCCTGGGAGTGGAGAGAGACAGTGC 1260  
DB 1204 TCTCTGCTGAGTGTGCTCTTAGCTCATTCCTGGGAGTGGAGAGAGACAGTGC 1263  
QY 1261 TTTTGTGGGATGCTCTAATCACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1320  
DB 1264 TTTTGTGGGATGCTCTAATCACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1323  
QY 1321 TGGACCTCATCCACTCTGTATGATCCACAGTGTCCAGACTAATTGTGACGAA 1380  
DB 1324 TGGACCTCATCCACTCTGTATGATCCACAGTGTCCAGACTAATTGTGACGAA 1383  
QY 1381 CTGAAATTAATAACCATCTACGATATCCAGGAAACAGAAACAGAGATGAGAGGA 1440  
DB 1384 CTGAAATTAATAACCATCTACGATATCCAGGAAACAGAAACAGAGATGAGAGGA 1443  
QY 1441 CAGGAAGCAGCTGGGACATTTAAAAATA 1472  
DB 1444 CAGGAAGCAGCTGGGACATTTAAAAATA 1475

## RESULT 12

US-10-063-513-79  
/ Sequence 79, Application US/10063513  
/ Publication No. US20030018172A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Baton, Dan L.  
/ APPLICANT: Rilveroff, Ellen  
/ APPLICANT: Gerilben, Mary E.  
/ APPLICANT: Goddard, Audrey  
/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, Christopher J.  
/ APPLICANT: Guiney, Austin L.  
/ APPLICANT: Metanabe, Colin K.  
/ APPLICANT: Wood, William I.  
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
/ FILE OF INVENTION: ACIDS ENCODING THE SAME  
/ FILE REFERENCE: P3230R1C1  
/ CURRENT APPLICATION NUMBER: US/10/063,513  
/ CURRENT FILING DATE: 2002-05-01  
/ Prior Application removed - See File Wrapper or Palm  
/ NUMBER OF SEQ ID NOS: 170  
/ SEQ ID NO 79  
/ LENGTH: 1475  
/ TYPE: DNA  
/ ORGANISM: Homo Sapien  
/ US-10-063-513-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAAGCTGGCAGAGAGACTGTGAATGAGGAGATTAGAGCTGTTCAGGAGCAAGA 60  
DB 4 AGAAGTCAAGCTGGCAGAGAGACTGTGAATGAGGAGATTAGAGCTGTTCAGGAGCAAGA 63  
QY 61 GCTTCAGCTGGAAGAGAGAGAGAGAGCTTCCCTGAAGAGCTTTCATGAGAGAGTCCCAT 120  
DB 64 GCTTCAGCTGGAAGAGAGAGAGAGAGCTTCCCTGAAGAGAGCTTTCATGAGAGAGTCCCAT 123  
QY 121 GGCCTCTCTTGGGCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 180  
DB 124 GGCCTCTCTTGGGCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 183  
QY 181 ACTGTTGCTCAGTCTCTCCAGCTGGAAGCAAGTCTTATGTCGGTCCAGCATTTGT 240  
DB 184 ACTGTTGCTCAGTCTCTCCAGCTGGAAGCAAGTCTTATGTCGGTCCAGCATTTGT 243  
QY 241 GACAGAGATTGGTTTCTCAAGGGCTCTGAGATGGAATGTCACACACAGCAGAGCAT 300

DB 244 GACAGAGATTGGTTTCTCAAGGGCTCTGAGATGGAATGTCACACACAGCAGAGCAT 303  
QY 301 CACCAAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATCCAGGCTGCCA 360  
DB 304 CACCAAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATCCAGGCTGCCA 363  
QY 361 GGCATGATGTGTACATCCAGTGCATTTCTCTCCCTGGGCTGATTAATCTCTGTGGG 420  
DB 364 GGCATGATGTGTACATCCAGTGCATTTCTCTCCCTGGGCTGATTAATCTCTGTGGG 423  
QY 421 CATGATGTCAGAGTCTTCTGCGAGGAATCCGAGCAAAAGACAGATGGGCTGACAG 480  
DB 424 CATGATGTCAGAGTCTTCTGCGAGGAATCCGAGCAAAAGACAGATGGGCTGACAG 483  
QY 481 TGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTTCTGTTGCTGAAATCTTCA 540  
DB 484 TGGAGTCTTTTTCATCTTGAAGGCTCTGGGATTCATTTCTGTTGCTGAAATCTTCA 543  
QY 541 TGGAGTCTTGAAGGATCTTCTACACACTGTGTGCTGACAGATGGAATTTGAGATTGG 600  
DB 544 TGGAGTCTTGAAGGATCTTCTACACACTGTGTGCTGACAGATGGAATTTGAGATTGG 603  
QY 601 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGCTGGAATCTTCC 660  
DB 604 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGCTGGAATCTTCC 663  
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTATGATGCTTCAACCAAGCCCA 720  
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCAACTATGATGCTTCAACCAAGCCCA 723  
QY 721 ACCTTTTGGCAGAGAGCTTCTCAGAGGCTGTGCACTTCCCAAGTCAAGATGATTT 780  
DB 724 ACCTTTTGGCAGAGAGCTTCTCAGAGGCTGTGCACTTCCCAAGTCAAGATGATTT 783  
QY 781 CAATTCCTACAGCTGACAGGATATGTGTAAGAAACAGAGGCTGAGAGCTGGGGGTGGC 840  
DB 784 CAATTCCTACAGCTGACAGGATATGTGTAAGAAACAGAGGCTGAGAGCTGGGGGTGGC 843  
QY 841 TGGGCTGTGAAACAGTGAAGAGACAGCCCGAGGAGCAGGTGAGGACATCACTACT 900  
DB 844 TGGGCTGTGAAACAGTGAAGAGACAGCCCGAGGAGCAGGTGAGGACATCACTACT 903  
QY 901 GATTCGTGCAAGAGTGTGCTGAGAGATGATGATCTTTGGGCAATTTGATGAGCAAG 960  
DB 904 GATTCGTGCAAGAGTGTGCTGAGAGATGATGATCTTTGGGCAATTTGATGAGCAAG 963  
QY 961 GCAGAAATGGGGCTAGTGAACAGATCAGATGTAATTTGCCAAGATGCTGCCATGC 1020  
DB 964 GCAGAAATGGGGCTAGTGAACAGATCAGATGTAATTTGCCAAGATGCTGCCATGC 1023  
QY 1021 CAGGCTTTTGTGTTTCTCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
DB 1024 CAGGCTTTTGTGTTTCTCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
QY 1081 GAAACCCCATTCCTTAAAGCAGAGATCAGAGATTCCTTTGGCTGTGTTTAACTGGG 1140  
DB 1084 GAAACCCCATTCCTTAAAGCAGAGATCAGAGATTCCTTTGGCTGTGTTTAACTGGG 1143  
QY 1141 ACTCATCCCAAAACCACTAATCAATCAATCCCACTGATGATGATGATGATGATGATGAT 1200  
DB 1144 ACTCATCCCAAAACCACTAATCAATCAATCCCACTGATGATGATGATGATGATGATGAT 1203  
QY 1201 TCTCTCTGCTGAGTGTGCTCTTAGCTATTTGTGGGATGGAGAGAGAGAGAGAGTGC 1260  
DB 1204 TCTCTCTGCTGAGTGTGCTCTTAGCTATTTGTGGGATGGAGAGAGAGAGAGAGTGC 1263  
QY 1261 TTTTGTGGGATTTGCTTAACTAATCTTGAAGCTTCCCTCAAGAACTGATTGGCCC 1320  
DB 1264 TTTTGTGGGATTTGCTTAACTAATCTTGAAGCTTCCCTCAAGAACTGATTGGCCC 1323  
QY 1321 TGGAACTTCATCCCACTCTGTATGATCCACAGTGTCCAGATGATGATGATGATGATGAT 1380  
DB 1324 TGGAACTTCATCCCACTCTGTATGATCCACAGTGTCCAGATGATGATGATGATGATGAT 1383





```

; GENERAL INFORMATION:
; APPLICANT: Balon, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritlsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P9230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIORITY FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-512-79

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Query Match      53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAAGTCAGCCTGGAGAGAGACTCTGAATAGAGGATAGAGGTTCAAGAGCAGA 60
DB 4 AGAAGTCAGCCTGGAGAGAGACTCTGAATAGAGGATAGAGGTTCAAGAGCAGA 63
QY 61 GCTTCAAGCTGAAAGACAGGAGAGAGCTCCCTGAAGAGCTTTTCTAGAGAGTCTGCAT 120
DB 64 GCTTCAAGCTGAAAGACAGGAGAGAGCTCCCTGAAGAGCTTTTCTAGAGAGTCTGCAT 123
QY 121 GGGCTCTCTGGCTCCCACTTGGGCTTCACTTGGGCTTCTGGGCTTTTGGGCTAC 180
DB 124 GGGCTCTCTGGCTCCCACTTGGGCTTCACTTGGGCTTCTGGGCTTTTGGGCTAC 183
QY 181 ACTGTTGACATCTGCTCCCAAGCTGGAAGACAGGTTTATGTCGGTCCAGCATTT 240
DB 184 ACTGTTGACATCTGCTCCCAAGCTGGAAGACAGGTTTATGTCGGTCCAGCATTT 243
QY 241 GACAGAGATGGCTTCTTCAAGGAGCTCTGATGGAATGTCACACACAGCAGCAT 300
DB 244 GACAGAGATGGCTTCTTCAAGGAGCTCTGATGGAATGTCACACACAGCAGCAT 303
QY 301 CACCCAGTGTGATCTATGACACCCCTTGGGCTGCGCTGACATCCAGGCTGCCA 360
DB 304 CACCCAGTGTGATCTATGACACCCCTTGGGCTGCGCTGACATCCAGGCTGCCA 363
QY 361 GGCATGATGTGATCACTGATGACACCCCTTGGGCTGCGCTGACATCCAGGCTGCCA 420
DB 364 GGCATGATGTGATCACTGATGACACCCCTTGGGCTGCGCTGACATCCAGGCTGCCA 423
QY 421 CATGATGATGACAGTCTTCTGCAAGATCCCAAGACCAAGACAGTGGCGTACAGG 480
DB 424 CATGATGATGACAGTCTTCTGCAAGATCCCAAGACCAAGACAGTGGCGTACAGG 483
QY 481 TGAAGCTTTTATCTTGAAGGCTCTGGAATTCATCTGTTGCTGGAATCTTCA 540
DB 484 TGAAGCTTTTATCTTGAAGGCTCTGGAATTCATCTGTTGCTGGAATCTTCA 543
QY 541 TGGGATCTTACGAGGACTTCTACTACACAGCTGATGCTGACAGATGAATTTGAGATTGG 600
DB 544 TGGGATCTTACGAGGACTTCTACTACACAGCTGATGCTGACAGATGAATTTGAGATTGG 603
QY 601 AGAGGCTCTTACTTGGGCAATTAATTTCTTCTGTTCTCCCTGATGATGCTGAAATCATCT 660
DB 604 AGAGGCTCTTACTTGGGCAATTAATTTCTTCTGTTCTCCCTGATGATGCTGAAATCATCT 663
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCTCACTATAGATGCTTACCAAGCCCA 720

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DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTCTCACTATAGATGCTTACCAAGCCCA 723
QY 721 ACCTTGGCCACAGAGAGCTCTCCAAAGGCTGCTCAACCTCCCAAGATGAGTGT 780
DB 724 ACCTTGGCCACAGAGAGAGCTCTCCAAAGGCTGCTCAACCTCCCAAGATGAGTGT 783
QY 781 CAATTCCTACAGCTGACAGGATATGTTGAGAGACCAAGGAGCCAGAGCTGGGGGTTGGC 840
DB 784 CAATTCCTACAGCTGACAGGATATGTTGAGAGACCAAGGAGCCAGAGCTGGGGGTTGGC 843
QY 841 TGGGCTGGAAGAAACAGTGAAGAGACCCCGAGGGCCACAGGTGAGGACATCACT 900
DB 844 TGGGCTGGAAGAAACAGTGAAGAGACCCCGAGGGCCACAGGTGAGGACATCACT 903
QY 901 GGATGCTGTCAGAGGCTGCTGAGAGATGACTGATCTTGGCCATTTGATGAGCAAG 960
DB 904 GGATGCTGTCAGAGGCTGCTGAGAGATGACTGATCTTGGCCATTTGATGAGCAAG 963
QY 961 GCAAGAAATGGGGCTTATGTAACAGATGACAGTTGAATTTGCCAAGATGCTGCCATGC 1020
DB 964 GCAAGAAATGGGGCTTATGTAACAGATGACAGTTGAATTTGCCAAGATGCTGCCATGC 1023
QY 1021 CAGCTTTTCTGTTTCTCTACCTTGGCTGCCCTGCCCTGAGTCCCAACCTCACT 1080
DB 1024 CAGCTTTTCTGTTTCTCTACCTTGGCTGCCCTGCCCTGAGTCCCAACCTCACT 1083
QY 1081 GAAACCCCATTCCTTAAAGCAGAGCTCAGAGATCCCTTGGCTCTGATTAAGTGGG 1140
DB 1084 GAAACCCCATTCCTTAAAGCAGAGCTCAGAGATCCCTTGGCTCTGATTAAGTGGG 1143
QY 1141 ACTTCATCCCAACCACTTATACATCCATCCATGACTGACCTCTGTGATCAAAAGCC 1200
DB 1144 ACTTCATCCCAACCACTTATACATCCATCCATGACTGACCTCTGTGATCAAAAGCC 1203
QY 1201 TCTCTGCTGAGTGTGCTGCTTACCTGATCTGCTGAGGAGTGGAGAGACAGTGGC 1260
DB 1204 TCTCTGCTGAGTGTGCTGCTTACCTGATCTGCTGAGGAGTGGAGAGACAGTGGC 1263
QY 1261 TTTTGTGGGATTTGCTTAACTTCTTCAAGCTTCCCTCAAGAAACATGATTTGGCCC 1320
DB 1264 TTTTGTGGGATTTGCTTAACTTCTTCAAGCTTCCCTCAAGAAACATGATTTGGCCC 1323
QY 1321 TGAACCTCATTCCTCACTCTTGTATGACTCCCAAGTGTCCAGATTAATTTGATGAA 1380
DB 1324 TGAACCTCATTCCTCACTCTTGTATGACTCCCAAGTGTCCAGATTAATTTGATGAA 1383
QY 1381 CTGAATTAACCACTCTTACGATATCCAGGAAACAGAAAGCAGATGAGATGGAGGA 1440
DB 1384 CTGAATTAACCACTCTTACGATATCCAGGAAACAGAAAGCAGATGAGATGGAGGA 1443
QY 1441 CAGGAAGGAGCCTGGGACATTTAAAAAATA 1472
DB 1444 CAGGAAGGAGCCTGGGACATTTAAAAAATA 1475

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RESULT 15
US-10-121-049-491
; Sequence 491, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritlsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

```

APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C17  
CURRENT APPLICATION NUMBER: US/10/121,049  
PRIORITY FILING DATE: 2002-04-12  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 491  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-121-049-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGCGACAGAGACTCTGAATGAGGATTAGAGTTTCAAGAGCAAGA 60  
DB 4 AGAAGTACGCTGCGACAGAGACTCTGAATGAGGATTAGAGTTTCAAGAGCAAGA 63  
QY 61 GCTTCAGCTGGAAGCAAGGAGAGGATCCCTGAAGAGGCTTCTAGAGAGGTTGCGCAT 120  
DB 64 GCTTCAGCTGGAAGCAAGGAGAGGATCCCTGAAGAGGCTTCTAGAGAGGTTGCGCAT 123  
QY 121 GGCCTCTCTGCGCTCCCACTTGTGGGCTACATCTAGAGGCTTGTGGGCTTTTGGGCA 180  
DB 124 GGCCTCTCTGCGCTCCCACTTGTGGGCTACATCTAGAGGCTTGTGGGCTTTTGGGCA 183  
QY 181 ACTGTTGCGCATGCTGCTCCCACTGGAAGCAAGTTCTTATGTGGTGCAGCATTTGT 240  
DB 184 ACTGTTGCGCATGCTGCTCCCACTGGAAGCAAGTTCTTATGTGGTGCAGCATTTGT 243  
QY 241 GACAGAGTGGGCTTCTCAAGGAGGCTCTGGAAGGAAATGTCACACAGACAGAGGAT 300  
DB 244 GACAGAGTGGGCTTCTCAAGGAGGCTCTGGAAGGAAATGTCACACAGACAGAGGAT 303  
QY 301 CACCAAGTGTGACATCTATAGCACTTGTGGGCTGCGCGCTGACATCCAGGCTGCGCA 360  
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QY 361 GGCATATAGTGTGACATCCAGGATCTCTCCCTGCGCTGCAATCTTGTGTGGG 420  
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QY 421 CATGAGATGACAGTCTTGTGCGCAGGAATCCCGAGCAAGAGACAGAGTGGGATGAG 480  
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DB 724 ACTCTTTCACAGAGAGCTCTCAAGGCTGCTCAACCTCCAAAGTCAAGATGAGTT 783

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DB 784 CAATTCCTACAGCCTGACAGGATATGTGTGAAGAACCAAGGAGCTGAGGAGTGGC 843  
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QY 901 GGAATGTCAGAGAGGCTGTGAGATGACTGATCTTGTGGCAATTTGAGCAAG 960  
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QY 1321 TGAACCTCATCCCACTCTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1380  
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QY 1381 CTGAATTAACCACTCTTATGATGACTCAAGGAGACAGAAAGCAGATGAGTGGAGGA 1440  
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QY 1441 CAGGAGGAGGCTGAGGACATTTAAAAAATA 1472  
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Search completed: October 30, 2004, 19:06:02  
Job time : 1797 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:21:12 ; Search time 131 Seconds

(without alignments)  
569.234 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174

Sequence: 1 MASIGQLVGYIIGLGLG.....PGQPKVKSEFNSYSLGYV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1174	100.0	230	10	US-09-998-598-2590
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13	1174	100.0	230	10	US-09-998-598-2590

14	1174	100.0	230	14	US-10-063-515-80	Sequence 80, App1
15	1174	100.0	230	14	US-10-063-512-80	Sequence 80, App1
16	1174	100.0	230	14	US-10-121-049-492	Sequence 492, App
17	1174	100.0	230	14	US-10-123-904-492	Sequence 492, App
18	1174	100.0	230	14	US-10-140-470-492	Sequence 492, App
19	1174	100.0	230	14	US-10-063-502-80	Sequence 80, App1
20	1174	100.0	230	14	US-10-175-746-492	Sequence 492, App
21	1174	100.0	230	14	US-10-176-918-492	Sequence 492, App
22	1174	100.0	230	14	US-10-176-921-492	Sequence 492, App
23	1174	100.0	230	14	US-10-063-548-80	Sequence 80, App1
24	1174	100.0	230	14	US-10-137-865-492	Sequence 492, App
25	1174	100.0	230	14	US-10-140-474-492	Sequence 492, App
26	1174	100.0	230	14	US-10-142-431-492	Sequence 492, App
27	1174	100.0	230	14	US-10-143-114-492	Sequence 492, App
28	1174	100.0	230	14	US-10-140-002-492	Sequence 492, App
29	1174	100.0	230	14	US-10-063-554-80	Sequence 80, App1
30	1174	100.0	230	14	US-10-006-856A-134	Sequence 134, App
31	1174	100.0	230	14	US-10-142-419-492	Sequence 492, App
32	1174	100.0	230	14	US-10-063-553-80	Sequence 80, App1
33	1174	100.0	230	14	US-10-063-518-80	Sequence 80, App1
34	1174	100.0	230	14	US-10-123-262-492	Sequence 492, App
35	1174	100.0	230	14	US-10-142-423-492	Sequence 492, App
36	1174	100.0	230	14	US-10-063-598-80	Sequence 80, App1
37	1174	100.0	230	14	US-10-227-693-80	Sequence 80, App1
38	1174	100.0	230	14	US-10-006-818A-134	Sequence 134, App
39	1174	100.0	230	14	US-10-121-050-492	Sequence 492, App
40	1174	100.0	230	14	US-10-141-755-492	Sequence 492, App
41	1174	100.0	230	14	US-10-143-032-492	Sequence 492, App
42	1174	100.0	230	14	US-10-063-563-80	Sequence 80, App1
43	1174	100.0	230	14	US-10-006-485A-134	Sequence 134, App
44	1174	100.0	230	14	US-10-013-907A-134	Sequence 134, App
45	1174	100.0	230	14	US-10-015-499A-134	Sequence 134, App

#### ALIGNMENTS

RESULT 1  
US-09-998-598-2590  
Sequence 2590, Application US/09998598  
Patent No. US20020150922A1  
GENERAL INFORMATION:  
APPLICANT: Stolk, John A.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Chenault, Ruth A.  
APPLICANT: Meagher, Madeline Joy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.561  
CURRENT FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 2606  
SOFTWARE: Corixa Invention Disclosure Database  
SEQ ID NO 2590  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-998-598-2590  
Query Match 100.0%; Score 1174; DB 9; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3, 8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MASIGQLVGYIIGLGLGLTLVAMLLPSKTSYVAGASIVTAVGFSKGLMECATSTG 60  
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Db 61 ITTCDITSTLGLPADIOQAQAMVNTSSATSSACIISVGMCTVFCQSSRAKDRVAVA 120  
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Db 121 GGVEFIIIGLIGLIPVAMNHGILRDFSPVLPVDSMKFEIGALYIGIISLPSLIAGIT 180  
 Qy 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKYSSEFNSYSLTGYV 230  
 Db 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKYSSEFNSYSLTGYV 230

RESULT 2

US-09-888-257A-6  
 ; Sequence 6, Application US/09888257A  
 ; Publication No. US20030060612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Polakie, Paul  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Wu, Thomas D.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 ; TITLE OF INVENTION: TREATMENT OF TUMOR  
 ; FILE REFERENCE: P5002R1  
 ; CURRENT APPLICATION NUMBER: US/09/888, 257A  
 ; PRIOR APPLICATION NUMBER: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/063, 540  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: US 60/089, 653  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 60/099, 792  
 ; PRIOR FILING DATE: 1998-09-10  
 ; PRIOR APPLICATION NUMBER: US 60/103, 678  
 ; PRIOR FILING DATE: 1998-10-08  
 ; PRIOR APPLICATION NUMBER: US 60/235, 451  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: 1999-06-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20111  
 ; PRIOR FILING DATE: 1999-09-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04342  
 ; PRIOR FILING DATE: 2000-02-18  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: 2000-03-30  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: 2000-12-01  
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 ; PRIOR FILING DATE: 2001-03-01  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SEQ ID NO 6  
 ; LENGTH: 230  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-09-888-257A-6

Query Match 100.0%; Score 1174; DB 10; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASIGLQVGVYIIGLIGLIGLVAMLLPSMTSSYVGASITVAVGFSKGLMECATHTSTG 60  
 Db 1 MASIGLQVGVYIIGLIGLIGLVAMLLPSMTSSYVGASITVAVGFSKGLMECATHTSTG 60  
 Qy 61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVGMRCVFCQESRADQRYAVA 120  
 Db 61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVGMRCVFCQESRADQRYAVA 120

Qy 121 GGVEFIIIGLIGLIPVAMNHGILRDFSPVLPVDSMKFEIGALYIGIISLPSLIAGIT 180  
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 Db 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKYSSEFNSYSLTGYV 230

RESULT 3

US-09-946-374-134  
 ; Sequence 134, Application US/09946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deonoyers, Luc  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C1  
 ; CURRENT APPLICATION NUMBER: US/09/946, 374  
 ; PRIOR APPLICATION NUMBER: 2001-09-04  
 ; PRIOR APPLICATION NUMBER: 60/098716  
 ; PRIOR FILING DATE: 1998-09-01  
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 ; PRIOR FILING DATE: 1998-09-10  
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PRO 1356



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 PRIOR FILING DATE: 1998-10-21  
 PRIOR APPLICATION NUMBER: 60/105169  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105266  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105693  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105694  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1174; DB 10; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3 8e-110;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASIGLQVGYIIGLLGLCTVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
 Db 1 MASIGLQVGYIIGLLGLCTVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60



1	PRIOR FILING DATE:	1997-10-29
2	PRIOR APPLICATION NUMBER:	60/064215
3	PRIOR FILING DATE:	1997-10-29
4	PRIOR APPLICATION NUMBER:	60/082797
5	PRIOR FILING DATE:	1999-04-22
6	PRIOR APPLICATION NUMBER:	60/083495
7	PRIOR FILING DATE:	1999-04-29
8	PRIOR APPLICATION NUMBER:	60/085579
9	PRIOR FILING DATE:	1998-05-15
10	PRIOR APPLICATION NUMBER:	60/087759
11	PRIOR FILING DATE:	1999-06-02
12	PRIOR APPLICATION NUMBER:	60/088021
13	PRIOR FILING DATE:	1999-06-04
14	PRIOR APPLICATION NUMBER:	60/088029
15	PRIOR FILING DATE:	1999-06-04
16	PRIOR APPLICATION NUMBER:	60/088030
17	PRIOR FILING DATE:	1999-06-04
18	PRIOR APPLICATION NUMBER:	60/088734
19	PRIOR FILING DATE:	1999-06-10
20	PRIOR APPLICATION NUMBER:	60/088740
21	PRIOR FILING DATE:	1999-06-10
22	PRIOR APPLICATION NUMBER:	60/088811
23	PRIOR FILING DATE:	1999-06-10
24	PRIOR APPLICATION NUMBER:	60/088824
25	PRIOR FILING DATE:	1999-06-10
26	PRIOR APPLICATION NUMBER:	60/088825
27	PRIOR FILING DATE:	1999-06-10
28	PRIOR APPLICATION NUMBER:	60/088863
29	PRIOR FILING DATE:	1999-06-11
30	PRIOR APPLICATION NUMBER:	60/089105
31	PRIOR FILING DATE:	1998-06-12
32	PRIOR APPLICATION NUMBER:	60/089514
33	PRIOR FILING DATE:	1999-06-16
34	PRIOR APPLICATION NUMBER:	60/089653
35	PRIOR FILING DATE:	1999-06-17
36	PRIOR APPLICATION NUMBER:	60/089952
37	PRIOR FILING DATE:	1998-06-19
38	PRIOR APPLICATION NUMBER:	60/090246
39	PRIOR FILING DATE:	1999-06-22
40	PRIOR APPLICATION NUMBER:	60/090444
41	PRIOR FILING DATE:	1999-06-24
42	PRIOR APPLICATION NUMBER:	60/090688
43	PRIOR FILING DATE:	1999-06-25
44	PRIOR APPLICATION NUMBER:	60/090656
45	PRIOR FILING DATE:	1999-06-25
46	PRIOR APPLICATION NUMBER:	60/090862
47	PRIOR FILING DATE:	1999-06-26
48	PRIOR APPLICATION NUMBER:	60/091628
49	PRIOR FILING DATE:	1998-07-02
50	PRIOR APPLICATION NUMBER:	60/096012
51	PRIOR FILING DATE:	1999-08-10
52	PRIOR APPLICATION NUMBER:	60/096757
53	PRIOR FILING DATE:	1999-08-17
54	PRIOR APPLICATION NUMBER:	60/096949
55	PRIOR FILING DATE:	1999-08-18
56	PRIOR APPLICATION NUMBER:	60/096959
57	PRIOR FILING DATE:	1999-08-18
58	PRIOR APPLICATION NUMBER:	60/097954
59	PRIOR FILING DATE:	1999-08-26
60	PRIOR APPLICATION NUMBER:	60/097971
61	PRIOR FILING DATE:	1998-08-26
62	PRIOR APPLICATION NUMBER:	60/097979
63	PRIOR FILING DATE:	1999-08-26
64	PRIOR APPLICATION NUMBER:	60/098749
65	PRIOR FILING DATE:	1999-09-01
66	PRIOR APPLICATION NUMBER:	60/099741
67	PRIOR FILING DATE:	1999-09-10
68	PRIOR APPLICATION NUMBER:	60/099763
69	PRIOR FILING DATE:	1999-09-10
70	PRIOR APPLICATION NUMBER:	60/099792
71	PRIOR FILING DATE:	1999-09-10
72	PRIOR APPLICATION NUMBER:	60/099812
73	PRIOR FILING DATE:	1999-09-10

PRIOR APPLICATION NUMBER: 60/0989815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-20
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106030
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106454
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106856
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108070
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/112419
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112853
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113011
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/112854
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113408
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114223
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/115614
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115527
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/119285

PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/119287  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/119525  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/120014  
PRIOR FILING DATE: 1999-02-11  
PRIOR APPLICATION NUMBER: 60/129122  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/129674  
PRIOR FILING DATE: 1999-04-16  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/144791  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/199397  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/380139  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 1174; DB 13; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCRSCSSQRRNSNYDAYOAOPLATRSSPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCRSCSSQRRNSNYDAYOAOPLATRSSPRGQPPVKSEFNSYSLTGYV 230

## RESULT 7

US-10-063-547-80  
Sequence 80; Application US/10063547  
Publication No. US2002018263A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-10-063-547-80

Query Match 100.0%; Score 1174; DB 13; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCRSCSSQRRNSNYDAYOAOPLATRSSPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCRSCSSQRRNSNYDAYOAOPLATRSSPRGQPPVKSEFNSYSLTGYV 230

## RESULT 8

US-10-063-551-80  
Sequence 80; Application US/10063551  
Publication No. US2002018349A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,551  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-10-063-551-80

Query Match 100.0%; Score 1174; DB 13; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLFIPVAMNLHGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGII 180

Db 121 GGVFFILGLGFIPLVAMNHLGILRDFYSLVPSDKMFIEGALYGLTISLFFLGLGII 180  
Qy 181 LCPSCSQRNRSNYYDAYOAOPLATRSSPRGQPKKSEFNSYSLTGYV 230  
Db 181 LCPSCSQRNRSNYYDAYOAOPLATRSSPRGQPKKSEFNSYSLTGYV 230

## RESULT 9

US-10-028-072-492  
; Sequence 492, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028, 072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059836  
; PRIOR FILING DATE: 1997-09-24  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062285  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062814  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/062816  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063082  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/063127  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063327

; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063329  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063550  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063561  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063704  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063733  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063735  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063738  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064248  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/064809  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065846  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/066453  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/069212  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069278  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069334  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069694  
; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/072320  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: 60/073612  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081695  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081818  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082999  
; PRIOR FILING DATE: 1998-04-24





APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C182  
CURRENT APPLICATION NUMBER: US/10/140,808  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 492  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-808-492

Query Match 100.0%; Score 1174; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230

## RESULT 12

US-10-063-569-80  
Sequence 80, Application US/10063569  
Publication No. US20030018168A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,569  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-569-80

Query Match 100.0%; Score 1174; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230

## RESULT 13

US-10-063-513-80  
Sequence 80, Application US/10063513  
Publication No. US20030018172A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,513  
CURRENT FILING DATE: 2002-05-01  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-513-80

Query Match 100.0%; Score 1174; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGHPADIQAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGLGFIPIVAMNLHGILRDFYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYQAQPLATRSSPRGQPPVKSEFNSYSLTGYV 230

## RESULT 14

US-10-063-515-80  
Sequence 80, Application US/10063515  
Publication No. US20030018173A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Katanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-80

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Best Local Similarity 100.0%; Pred. No. 3 8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
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QY 61 ITCCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMRCCTVFCQESRAKDRVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMRCCTVFCQESRAKDRVAVA 120
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DB 121 GGVPFLLGGLGFIPIVAMNLHGILRDYSPPLVPSDKMKEIGEALYLGIIISLFSLIAGII 180
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RESULT 15
US-10-063-512-80
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; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Batton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Katanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
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; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-80
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Query Match          100.0%; Score 1174; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 3 8e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
DB 1 MASIGLQLVGYIIGLIGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60
QY 61 ITCCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMRCCTVFCQESRAKDRVAVA 120
DB 61 ITCCDIYSTLLGLPADIOAQAAMMTSSAISLACIISVGMRCCTVFCQESRAKDRVAVA 120
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DB 181 LCFSSCSQRNRNSNYDAYOQPLATRSSPRPGQPPKVKSEFNYSYLTGYV 230
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Search completed: October 27, 2004, 07:33:03  
Job time : 133 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:46:20 ; Search time 18347 Seconds  
(Without alignments)  
7067.551 Million cell updates/sec

Title: US-09-787-677A-7  
Perfect score: 2742  
Sequence: 1 agaagtcagccgcgcagaga.....ggtgatcataatctgtagc 2742

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues  
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBml:.\*  
1: gb ba:.\*  
2: gb htg:.\*  
3: gb\_in:.\*  
4: gb\_cm:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
9: gb\_dr:.\*  
10: gb\_ro:.\*  
11: gb\_ste:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2721.4	99.2	2959	9	AK075405 Homo sapi
3	2721.4	99.2	109465	9	AL158821 Human DNA
4	2715	99.0	2863	6	AX136129 Sequence
5	2715	99.0	2863	6	BD123517 Secretory
6	2715	99.0	2863	9	AK075371 Homo sapi
7	1482.8	54.1	1506	9	BC014424 Homo sapi
8	1482.8	54.1	1918	9	AF177340 Homo sapi
9	1472	53.7	1475	6	AX092348 Sequence
10	1472	53.7	1475	6	AK299996 Sequence
11	1472	53.7	1475	6	AX395213 Sequence
12	1472	53.7	1475	6	AX454606 Sequence
13	1472	53.7	1475	6	AX464358 Sequence
14	1472	53.7	1475	6	AX491084 Sequence
15	1472	53.7	1475	6	AK697065 Sequence
16	1472	53.7	1475	6	AY358474 Homo sapi
17	1453.4	53.0	1524	6	AR340718 Sequence
18	1453.4	53.0	1524	6	BD085897 Elongatio
19	1408.8	51.4	1441	6	AX286822 Sequence

20	1393.6	50.8	1400	6	AR340765 Sequence
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22	1043	38.0	184872	10	AL672243 Mouse DNA
23	1039.8	37.9	28828	10	BC015252 Mus muscu
24	955.8	34.9	239385	2	AC109686 Rattus no
25	955.8	34.9	250600	2	AC136646 Rattus no
26	955.8	34.9	268828	2	AC091513 Rattus no
27	937.4	34.2	1618	4	AB115779 Bos tauru
28	756.2	27.6	1032	4	AF358907 Canis fam
29	696	25.4	953	4	CO132222 Sequence
30	693	25.3	693	6	AF250558 Homo sapi
31	693	25.3	693	9	AF250558 Homo sapi
32	689.8	25.2	693	6	AX497200 Sequence
33	622.8	22.7	735	11	BV208439 ClDN2 226
34	611	22.3	779	6	AX286824 Sequence
35	611	22.3	791	6	E31591 E31591 Tight junct
36	611	22.3	791	10	AF072128 Mus muscu
37	477	17.4	615	6	AX136475 Sequence
38	477	17.4	615	6	BD123715 Secretory
39	401.2	14.6	405	6	AX939252 Sequence
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41	334	12.2	1492	5	BX934932 Gallus ga
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43	300	10.9	300	6	BD128818 Human gen
44	280.8	10.2	49323	2	AC107455 Mus muscu
45	266.6	9.7	324	6	AX939253 Sequence

#### ALIGNMENTS

RESULT 1	BD237562	2742 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD237562				
DEFINITION	Membrane-associated organized proteins.				
ACCESSION	BD237562.1	GI:33047332			
VERSION	BD237562.1	GI:33047332			
KEYWORDS	JP 2002525113-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Yue H., Lal P., Corley N.C., Guegler K.J., Baughn M.R., Lu A.D. and Tang T.Y.				
TITLE	Membrane-associated organized proteins				
JOURNAL	Patent: JP 2002525113-A 3 13-AUG-2002;				
COMMENT	INCYTE PHARMACEUTICALS INC				
OS	Homo sapiens (human)				
PN	JP 2002525113-A/3				
PD	13-AUG-2002				
PF	23-SEP-1999 JP 2000572362				
PR	25-SEP-1998 US 60/155215, 13-OCT-1998 US 60/155251 PR				
PI	HENRY YUE, PREETI LAL, NEIL C CORLEY, KARL J GUEGLER, MARIAN R PI BAUGHN.				
PC	AINA D LU, TOM Y TANG				
PC	C12N15/09, A61K38/00, A61K45/00, A61P1/00, A61P1/04, A61P3/00, A61P3/08,				
PC	A61P13/00, A61P13/12, A61P25/00, A61P29/00, A61P35/00, A61P37/00,				
PC	C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC				
PC	C12N21/02, C12Q1/68,				
CC	C12N15/00, C12N5/00, A61K37/02				
CC	Incyte ID No: 2594049CB1				
FT	Key	Location/Qualifiers			
FT	source	1. 2742			
FEATURES	Location/Qualifiers				
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RESULT 3  
 AL158821  
 LOCUS 109465 bp DNA linear PRI 08-FEB-2002  
 DEFINITION Human DNA sequence from clone Rpl-75H8 on chromosome Xq22.3-23  
 containing the CLDN2 gene for claudin 2, the gene for a novel protein  
 similar to KIAA0136, a eukaryotic translation elongation factor 1  
 alpha 1 (EBF1A1) pseudogene and a Cpg island, complete sequence.  
 AL158821  
 VERSION AL158821.16 GI:14329875  
 KEYWORDS HTG; claudin; CLDN2; Cpg island; EBF1A1; KIAA0136.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 109465)  
AUTHORS Heath, P.  
TITLE Direct Submission  
JOURNAL Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbrey@sanger.ac.uk  
COMMENT On Jun 8, 2001 this sequence version replaced gi:14160908.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MJ3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chrx>

Rp1-75H8 is from the library RPCI-1 constructed by the group of Pletzer de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYRAC2

IMPORTANT: This sequence is not the entire insert of clone Rp1-75H8. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone Rp1-75H8 is at 1 in this sequence. The true left end of clone Rp13-383K5 is at 109366 in this sequence.

## FEATURES

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64. 1090  
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3685. 3716  
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match: ESTs: Em:AW107793 Em:AA345449 Em:BG164241  
Em:BG423208 Em:T86266 Em:BE304667 Em:BG951731 Em:AA639438  
Em:BB480970 Em:BG951371 Em:BG328625 Em:BG35755  
Em:BG951374 Em:AT790813 Em:AM006504 Em:BF819923  
Em:AT62767 Em:BB847585 Em:BI006997 Em:BG63552  
Em:AI685439 Em:AI949846 Em:BB845010 Em:BG65977 Em:T86158  
Em:BG469035 Em:AA976345 Em:AV604013 Em:AI659323  
Em:BF104997 Em:BB653578 Em:BG385562 Em:AI913916  
Em:BE048787 Em:AM083920 Em:AV647382 Em:AI685788  
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15618. 16068  
/note="L2 repeat: matches 1967. .2418 of consensus"  
complement (17526. .77002)





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DEFINITION	Sequence 51 from Patent BP1067182.		
ACCESSION	AXI36129		
VERSION	AXI36129.1	GI:14272537	
KEYWORDS			
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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.		
JOURNAL	Secretory protein or membrane protein Patent: BP 1067182-A 51-10-JUN-2001;		
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DEFINITION	Secretory protein or membrane protein.		
ACCESSION	BD123517		
VERSION	BD123517.1	GI:23218462	
KEYWORDS	JP 2002017376-A/26.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: JP 2002017376-A 26 22-JAN-2002; HELIX RESEARCH INSTITUTE		
COMMENT	OS Homo sapiens (human) PN JP 2002017376-A/26 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253173 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU PI SUGIYAMA, PI KOJI HAYASHI PC		
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PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC			
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Qy	421	CATGAGATGACAGTCTTCTTCCAGGAATCCGAGCCAAAGAACAAGTGGCGGTGACAG	480
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Db	593	TGGAATCTTTTTCATCTTGGAGGCTCTTGGGATTCATTCCTGTTGGCTTGGAAATCTTCA	652
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LOCUS	
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VERSION	AK075371
KEYWORDS	to Mus musculus Claudin-2 mRNA.
SOURCE	AK075371.1 GI:22761413
ORGANISM	oligo capping; f1s (full insert sequence).
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	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Oea,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
	Ibiki,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
	Nakamura,Y., Nagahari,K., Sugano,S. and Isegai,T.
TITLE	HRI human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2863)
AUTHORS	Isegai,T. and Yamamoto,J.
TITLE	Direct Submission
JOURNAL	Submitted (20-MAR-2002) Takao Isegai, Helix Research Institute,
	Genomix Laboratory, 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
	(E-mail:genomix@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
	HRI human cDNA sequencing project; cDNA 5' - 3'-end one pass
	sequencing, clone selection and full insert sequencing; Helix
	Research Institute (supported by Japan Key Technology Center etc.);
	cDNA library construction; Institute of Medical Science, University
	of Tokyo, Laboratory of Genome Structure, Human Genome Center.
COMMENT	

**FEATURES**

**SOURCE**

**CDS**

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## ORIGIN

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**REMARK**  
**COMMENT**

Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shervenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, J.S., Krzywicki, M.I., Skalka, U., Smalins, D.E., Scherich, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 1506)  
 Strausberg, R.  
 Direct Submission  
 Submitted (17-Sep-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada  
[info@cgsc.bc.ca](mailto:info@cgsc.bc.ca)  
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anna Petruscu, Anna Liisa Prabhu, Parvaneh Saedi, JR Santos, Angelique Scherich, Ursula Skalka, Duane Smalins, Jeff Stoct, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

**FEATURES**  
**source**

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 ACCESSION AF177340  
 VERSION AF177340.1 GI:10503979  
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 SOURCE  
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 Homo sapiens  
 Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qiu,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.  
 TITLE Novel human cDNA clone with function of inhibiting cancer cell growth  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1918)  
 AUTHORS Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qiu,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-AUG-1999) National Laboratory for Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie Tu Road, Shanghai 200032, P.R. China  
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ORIGIN  
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 Best Local Similarity 99.5%; Pred. No. 0;

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DB 462 GCTTCAAGCTGAAAGCAAGGAGAGAGCTGTAAGAGCTTTCTAAGAGGTTCGCAT 521

QY 121 GGCCTCTTGGCTCCCACTGTTGGGCTAATCTCAAGGCTTTGGGGCTTTTGGGAC 180

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DB 1242 TGGGCTGTAAGAAACAGTGAAGAGCAAGGAGGCTGAGGCTGAGGCTGAGGCT 1301

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LOCUS AX092348

DEFINITION Sequence 79 from Patent WO0116318.

ACCESSION AX092348

VERSION AX092348.1 GI:13444488

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

1 Baton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0116318-A 79 08-MAR-2001; Genentech, Inc. (US)

TITLE

JOURNAL

FEATURES

source

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QY 121 GGCCTCTTGGCTCCCACTGTTGGGCTAATCTCAAGGCTTTGGGGCTTTTGGGAC 180

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Db	244	GACAGCAGTTGGCTTCTTCCAAAGGCTCTGTGATGGAATGTGCCACACACAGCAGGAT	303
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Qy	361	GGCCATGATGATGACATCCAGTCAATCTCTCCCTGAGCTGCAATTAATCTGTGTGG	420
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Qy	781	CAATTCCTACAGCTGACAGGCTATGTGTGAAGACAGGCGCCAGAGCTGGGGGGTGGC	840
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ACCESSION AX299996			
VERSION AX299996.1 GI:17129473			
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REFERENCE			
1 Eaton, D.L., Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J.,			
Gurney, A.L., Tumas, D., Matanabe, C.K., Wood, W.I., and Zhang, Z.			
Compositions and methods for the treatment of immune related			
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JOURNAL			
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LOCUS AX395213 1475 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent WO20216429.
ACCESSION AX395213
VERSION AX395213.1 GI:21066244
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Goddard, A., Goddard, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Composition and methods for the diagnosis and treatment of tumor
Patent: WO 0216429-A 1 28-FEB-2002;
Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred.No.0;
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DEFINITION Sequence 491 from Patent WO0140466.  
ACCESSION AX464358  
VERSION AX464358.1 GI:21899195  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,  
Gao, W.Q., Gerlitsen, M.E., Goddard, A., Godowski, P.J., Gueney, A.L.,  
Sherwood, S., Smith, V., Stewart, T.A., Tuma, D., Watanabe, C.K.,  
Wood, W.L., and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 491 07-JUN-2001;  
Genentech Inc. (US)  
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source 1.1475  
Location/Qualifiers  
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ACCESSION AX491084  
VERSION AX491084.1 GI:22323879  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE  
AUTHORS  
1 Baker, K.P., Ferrera, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurey, A.L., Hillan, K.J., Marek, S.A., Pan, J.,  
Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 020690-A 191 03-JAN-2002;  
Genentech, Inc. (US)  
location/Qualifiers

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Source  
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Best Local Similarity 100.0%; Pred. No. 0;  
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QY 61 GCTTCAAGCTGAG 120  
DB 64 GCTTCAAGCTGAG 123  
QY 121 GGCCTCTCTGAGCTTCAACTTGTGGCTTCACTTGAAGCTTGTGGGCTTTTGGGAC 180

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DEFINITION AX697065  
ACCESSION AX697065.1 GI:29498042  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Bacon, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Geddes, P.J., Guney, A.L., Smith, V., Tunas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.P., Roy, M.A. and Matarabe, C.K.  
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Patent: WO 0078961-A 133 28-DEC-2000;  
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FEATURES  
source

ORIGIN  
Query Match 53.7%; Score 1472; DB 6; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 GGCCATGATGATGACATCCAGTCAATCTCTCCCTGGCCCTGATTAATCTGTGGTGGG 420  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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42	1472	53.7	1475	9	ADA19091	ADA19091	Human PRO
43	1472	53.7	1475	9	ADA61714	ADA61714	Homo sapi
44	1472	53.7	1475	9	ADB19499	ADB19499	Novel hum
45	1472	53.7	1475	9	ADB28040	ADB28040	CDNA enco

## ALIGNMENTS

RESULT 1	AAAI2585	AAAI2585 standard; cDNA; 2742 BP.
ID	AAAI2585;	
XX	25-JUL-2000	(first entry)
DT		
XX		
DE		CDNA encoding a membrane associated organizational protein (HUNCT).
XX		
XX		Human; membrane associated organizational protein; HUNCT;
KW		cell proliferative disorder; cancer; autoimmune disorder;
KW		inflammatory disorder; neurological disorder; developmental disorder;
KW		vesicle trafficking; reproductive disorder; gastrointestinal disorder;
KW		renal disorder; atherosclerosis; leukemia; rheumatoid arthritis;
KW		Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;
KW		irritable bowel syndrome; allergy; ss.
OS		Homo sapiens.
XX		
PH	Key	Location/Qualifiers
FT	CDS	119..811
FT		/*tag= a
FT		/product= "membrane associated organizational protein"
XX		
XX	WO200018915-A2.	
XX	06-APR-2000.	
PD		
XX		
PF	23-SEP-1999;	99WO-US022082.
XX		
PR	25-SEP-1998;	98US-0155215P.
PR	13-OCT-1998;	98US-0155215P.
PR	04-MAY-1999;	99US-0172228P.
XX		
PA	(INCY-)	INCYTE PHARM INC.
XX		
PI	Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;	
XX		
XX	WPI; 2000-293154/25.	
DR	P-PSDB; AAY84609.	
XX		
PT		Human membrane associated organizational protein and nucleic acid
PT		sequences useful in the diagnosis, treatment and prevention of cell



```

Db 1681 ACTCTAGGGGACCTGACCTGCTCTTGGCTTAACCAAGGCTTAGGGCTATAGCAAT 1740
Qy 1741 GGTTCCTTAGAAGACGTAACCAAGTTTCTAGGATGGCCCTTGCTGGGGATGACA 1800
Db 1741 GGTTCCTTAGAAGACGTAACCAAGTTTCTAGGATGGCCCTTGCTGGGGATGACA 1800
Qy 1801 GTGTGGAGCTGTGGGGTACTGAGGAAGACCAATTCCTTAGAGGTCTTAGAAGCCAG 1860
Db 1801 GTGTGGAGCTGTGGGGTACTGAGGAAGACCAATTCCTTAGAGGTCTTAGAAGCCAG 1860
Qy 1861 GTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Db 1861 GTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Qy 1921 AGAACTCTTAGAGCGTATAGAAATCAGCTCAATGAGTACAGGCCCCCGAGGGTCC 1980
Db 1921 AGAACTCTTAGAGCGTATAGAAATCAGCTCAATGAGTACAGGCCCCCGAGGGTCC 1980
Qy 1981 ACCCAGAGCACTACAGAGCCTCTGAAAGACATAGACCAAGCGGCCCTTCAGATT 2040
Db 1981 ACCCAGAGCACTACAGAGCCTCTGAAAGACATAGACCAAGCGGCCCTTCAGATT 2040
Qy 2041 CCCCACGTGTCCATCGGAGATGCTCCAGAGTGGCTAGAGGGCATCTAAGGGCTCCAGCA 2100
Db 2041 CCCCACGTGTCCATCGGAGATGCTCCAGAGTGGCTAGAGGGCATCTAAGGGCTCCAGCA 2100
Qy 2101 TGGCATATCCATGCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Db 2101 TGGCATATCCATGCCCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2161 GGGATTCAGCTAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2220
Db 2161 GGGATTCAGCTAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2220
Qy 2221 GTCCGAATATGTTCCCTTTACCTCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 2280
Db 2221 GTCCGAATATGTTCCCTTTACCTCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 2280
Qy 2281 TCCCTCAGCAGTGTAGGATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Db 2281 TCCCTCAGCAGTGTAGGATGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
Qy 2341 CATTTGACAGAGAGAGGGCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 CATTTGACAGAGAGAGGGCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Qy 2401 TTGCCATGTTCCAGCTGCTCTCTCCCACTGGAAGCCGCTCTCCCTTAGCCAGTCTCC 2460
Db 2401 TTGCCATGTTCCAGCTGCTCTCTCCCACTGGAAGCCGCTCTCCCTTAGCCAGTCTCC 2460
Qy 2461 TCAGGCTTGGAGAACTTCTCAGCGTCACTCTTCATGTAGAGCTTCTGTAGTCACTCA 2520
Db 2461 TCAGGCTTGGAGAACTTCTCAGCGTCACTCTTCATGTAGAGCTTCTGTAGTCACTCA 2520
Qy 2521 TCCCTCTCCCAACCCCTCCCTCCCAACCCCTCCCAACCCCTCCCAACCCCTCCCAACCC 2580
Db 2521 TCCCTCTCCCAACCCCTCCCTCCCAACCCCTCCCAACCCCTCCCAACCCCTCCCAACCC 2580
Qy 2581 CATTCACAAATTTTGTATGATGCTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Db 2581 CATTCACAAATTTTGTATGATGCTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Qy 2641 GTAAACCTTCGGTGGGTGGGGCCATATCTTAGACCTTCTGTATCCCCCAAGCTATCT 2700
Db 2641 GTAAACCTTCGGTGGGTGGGGCCATATCTTAGACCTTCTGTATCCCCCAAGCTATCT 2700
Qy 2701 GTAAACCTTCGGTGGGTGGGGCCATATCTTAGACCTTCTGTATCCCCCAAGCTATCT 2742
Db 2701 GTAAACCTTCGGTGGGTGGGGCCATATCTTAGACCTTCTGTATCCCCCAAGCTATCT 2742

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AAFP3769
ID AAFP3769 standard; cDNA; 2863 BP.
AC AAFP3769;
XX
XX
XX 23-MAY-2001 (first entry)
DE Human cDNA encoding a membrane or secretory protein clone PSEC0059.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
XX rheumatoid arthritis; diabetes; ss.
OS Homo sapiens.
XX
XX EP1067182-A2.
PD 10-JAN-2001.
XX
XX 07-JUL-2000; 2000EP-00114090.
XX
XX 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
PA
PI Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX WPI; 2001-093989/11.
DR P-PSDB; AAB88342.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
XX Claim 1; SEQ ID NO 51; 603pp + Sequence listing; English.
XX
XX This invention relates to nucleic acid sequences AAFP3744 - AAFP3916
XX which encode human secretory or membrane proteins represented by AAB88317
XX - AAB88419. Included in the invention are primers AAFP3917 - AAFP4295 and
XX AAFP6232 - AAFP6235 which are used to isolate the cDNA sequences of the
XX invention. The invention also includes methods for the production of
XX antibodies directed against the proteins, and cDNA sequences, which can
XX be used in vaccines. The polynucleotide sequences can be used in gene
XX therapy. The polynucleotide sequences and the proteins they encode may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate secretory protein/membrane protein expression. The
XX nucleic acids and complementary sequences may also be used as DNA probes
XX in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
XX and quantitate the presence of similar nucleic acid sequences in samples.
XX They may also be used to study the expression and function of secretory
XX proteins/membrane polypeptides and their role in metabolism. The
XX polypeptides may be used as antigens in the production of antibodies
XX against them and in assays to identify modulators (agonists and
XX antagonists) of expression and activity. The antibodies and antagonists
XX may also be used as therapeutic agents to down regulate expression and
XX activity. The antibodies may also be used as diagnostic agents for
XX detecting the presence of the polypeptides in samples (e.g. by enzyme
XX linked immunosorbent assay (ELISA)). Examples of diseases which may be
XX treated include rheumatoid arthritis and diabetes
XX
XX Sequence 2863 BP; 670 A; 794 C; 711 G; 688 T; 0 U; 0 Other;
SQ
Query Match 99.0%; Score 2715; DB 5; Length 2863;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 AGAAGTCAGCTGAGAGAGAGCTCTGAATGAGGATTTAGAGTGTTCAGAGAGCAGA 60
Db 113 AGAAGTCAGCTGAGAGAGAGCTCTGAATGAGGATTTAGAGTGTTCAGAGAGCAGA 172
Qy 61 GCTTCAGCTGAGAGAGAGAGAGAGCTCTGAGAGAGCTTCTACTAGAGGTCTGCGCAT 120
Db 173 GCTTCAGCTGAGAGAGAGAGAGAGAGCTCTGAGAGAGCTTCTACTAGAGGTCTGCGCAT 232

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Db	2393	TCCTCAACCACTCTAAGGCATATCGGCTTCTGAAAAATTCAGACACACTTCTGAACT	2452
Qy	2341	CATTGTGACGAGAGGGCCCATCTGTGTCTGTAAACAATGCTTTCACATGTCCACCTTC	2400
Db	2453	CATTGTGACGAGAGGGCCCATCTGTGTCTGTAAACAATGCTTTCACATGTCCACCTTC	2512
Qy	2401	TTGGCATTGTTCAAGCTGCTCTCCCAACTGGAAAGGCGGTCTCCCTTAGCCAACTCTCC	2460
Db	2513	TTGGCATTGTTCAAGCTGCTCTCCCAACTGGAAAGGCGGTCTCCCTTAGCCAACTCTCC	2572
Qy	2461	TCAGGCTTGGAACTTCCTCAAGGTACCTTCCTTCAATGAGCCCTCTCTGATACATCCA	2520
Db	2573	TCAGGCTTGGAACTTCCTCAAGGTACCTTCCTTCAATGAGCCCTCTCTGATACATCCA	2632
Qy	2521	TCCCTTCCTCAACCCCTCCCTCCCAACCCCTCAATGTATAATTGCTCTTGATGCTTAG	2580
Db	2633	TCCCTTCCTCAACCCCTCCCTCCCAACCCCTCAATGTATAATTGCTCTTGATGCTTAG	2652
Qy	2581	CATTCACAATTTTGAATGATCGTATTATGTGTGTGTGTCCGATCTCAACAATATATT	2640
Db	2693	CATTCACAATTTTGAATGATCGTATTATGTGTGTGTGTCCGATCTCAACAATATATT	2752
Qy	2641	GTAACCCCTTCGGTGGTGGGGGCCATATCTTAAGACTCTCTGTATCCCAAGACTATCT	2700
Db	2753	GTAACCCCTTCGGTGGTGGGGGCCATATCTTAAGACTCTCTGTATCCCAAGACTATCT	2812
Qy	2701	GTAACAGTCCAGGACACACAAAGTGATCAATAA	2734
Db	2813	GTAACAGTCCAGGACACAGATGAAGTATCAATAA	2847

RESULT 3  
 ACC50950  
 ID ACC50950 standard; cDNA, 3126 BP.  
 XX  
 AC ACC50950;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human secreted protein BAC clone SEQ ID NO 1130.  
 XX  
 KW Cardiac; antiarrhythmic; antiarteriosclerotic; vasotrophic; cytostatic;  
 KW vulnerable; antiinflammatory; neurotropic; neuroprotective;  
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200295010-A2.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 19-MAR-2002; 2002WO-US009785.  
 XX  
 PR 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 PA (HUMA-) HUMAN GENOME SCT INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 WP; 2003-129429/12.  
 XX  
 PT Novel human secreted proteins, useful for detecting, preventing,  
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular  
 PT disorders such as arrhythmia.  
 XX  
 PS Disclosure; SEQ ID NO 1130; 1881bp; English.  
 CC The present invention relates to novel human secreted proteins (ABR47633-  
 CC ABR8145) and their coding sequences (ACC50344-ACC50856). The proteins  
 CC and their coding sequences are useful for the preparation of a diagnostic

Query Match	99.0%	Score 2715	DB 8	Length 3126
Best Local Similarity	99.8%	Prod. No. 0		
Matches 2729	Conservative	0	Mismatches 5	Indels 1
Gaps	1			
QY	1	AGAAGTCAGCCCTGGAGAGAGACTCTGAAATGAGGAGATTAGAGGTTCAAGAGACAGAGA	60	
Db	373	AGAACTCAGCCCTGGAGAGAGACTCTGAAATGAGGAGATTAGAGGTTCAAGAGACAGAGA	432	
QY	61	GCTTCAGCCTGAAGACAAGAGAGAGAGCTCTGAAGACGCTTTACTAGAGAGCTTCGCAT	120	
Db	433	GCTTCAGCCTGAAGACAAGAGAGAGAGCTCTGAAGACGCTTTACTAGAGAGCTTCGCAT	492	
QY	121	GGCCTCTCTTGGCCTTCACATTTGAGGCTACATCCTAGGCTCTTGGGGCTTTGGGCAC	180	
Db	493	GGCCTCTCTTGGCCTTCACATTTGAGGCTACATCCTAGGCTCTTGGGGCTTTGGGCAC	552	
QY	181	ACTGTTGTCAGATGCTGCTCCCGAGCTGGAAAACAAGTCTTATATGCGGTGCAGATTGT	240	
Db	553	ACTGTTGTCAGATGCTGCTCCCGAGCTGGAAAACAAGTCTTATATGCGGTGCAGATTGT	612	
QY	241	GACAGCAGTTGAGCTTCTCAAGAGGCTCTGAGTGAATGATGTCACACACAGACAGGCAT	300	
Db	613	GACAGCAGTTGAGCTTCTCAAGAGGCTCTGAGTGAATGATGTCACACACAGACAGGCAT	672	
QY	301	CACCCAGTGTACATCTVAVAGACCCCTTCTGAGGCTGCGCCGCTGACATCCAGGCTGCCA	360	
Db	673	CACCCAGTGTACATCTVAVAGACCCCTTCTGAGGCTGCGCCGCTGACATCCAGGCTGCCA	732	
QY	361	GGCCATATGATGATCATTCAGTGAATCTCTCCCTGGCCGTCATTAATCTGATGATGGG	420	
Db	733	GGCCATATGATGATCATTCAGTGAATCTCTCCCTGGCCGTCATTAATCTGATGATGGG	792	
QY	421	CATGAGATGACAGTCTCTGCGACAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	480	
Db	793	CATGAGATGACAGTCTCTGCGACAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG	852	
QY	481	TGAGCTCTTTTTCATCTTGAAGGCTCTGGAGATTCAATCTGTTGCTTGAATCTTCA	540	
Db	853	TGAGCTCTTTTTCATCTTGAAGGCTCTGGAGATTCAATCTGTTGCTTGAATCTTCA	912	
QY	541	TGGATCTCTAAGGAGCTTCTAATGACCATGATGCTGACAGCATGAATTTGAAATGG	600	
Db	913	TGGATCTCTAAGGAGCTTCTAATGACCATGATGCTGACAGCATGAATTTGAAATGG	972	
QY	601	AGAGGCTCTTTAATCTTGGGCAATTAATTTCTCCCTGTTCTCCGATAGCTGAAATCATCT	660	
Db	973	AGAGGCTCTTTAATCTTGGGCAATTAATTTCTCCCTGTTCTCCGATAGCTGAAATCATCT	1033	
QY	661	CTGCTTTTCTGCTCATCCAGAGAAATCGCTCAACTAATGATGCTTACAAAGCCCA	720	

Db 1033 CTGCTTTCTGCTCATCCAGAGAAATGCTCCACCTACATCATCCACCAAGCCCA 1092  
Qy 721 ACCCTTGCCACAAGAGCTCTCCAGAGCCCTGCTCACTCCCAAGTCAAGAGTGT 780  
Db 1093 ACCTCTTGCCACAAGAGCTCTCCAGAGCCCTGCTCACTCCCAAGTCAAGAGTGT 1152  
Qy 781 CAATTCCTACAGCTGACAGGGATATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGC 840  
Db 1153 CAATTCCTACAGCTGACAGGGATATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGC 1212  
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Db 1273 GGAATGCTGAGAAAGTGTGCTGAGAGTGAATGCTTTGGCCATTTGGAATTGAGCAAG 1332  
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGATGCAAGTGAATTGCCAAGATGCTGCATGC 1020  
Db 1333 GCAGAAATGGGGGCTAGTGTAAACAGATGCAAGTGAATTGCCAAGATGCTGCATGC 1392  
Qy 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCACTT 1080  
Db 1393 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCACTT 1452  
Qy 1081 GAAACCCCATTCCTCTTAAGCAGAGCTCAGAGGATCCCTTGGCCCTGAGTTAACTGGG 1140  
Db 1453 GAAACCCCATTCCTCTTAAGCAGAGCTCAGAGGATCCCTTGGCCCTGAGTTAACTGGG 1512  
Qy 1141 ACTCCATCCCAAAACCCCATTAATCAATCCCATGCTGACCTCTGTGATCAAAAGACC 1200  
Db 1513 ACTCCATCCCAAAACCCCATTAATCAATCCCATGCTGACCTCTGTGATCAAAAGACC 1572  
Qy 1201 TCTCTCTGCTGAGTGTGCTCTTAAGTCAATGCTGGGGATGGGAAAGAAAGAGTGGC 1260  
Db 1573 TCTCTCTGCTGAGTGTGCTCTTAAGTCAATGCTGGGGATGGGAAAGAAAGAGTGGC 1632  
Qy 1261 TTTTGTGGGCAATTGCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATTTGACC 1320  
Db 1633 TTTTGTGGGCAATTGCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATTTGACC 1692  
Qy 1321 TGGAACTCCATCCCATCTCTTTGATGATCCACAGTGTCCAGATTAATTTGTGCATGAA 1380  
Db 1693 TGGAACTCCATCCCATCTCTTTGATGATCCACAGTGTCCAGATTAATTTGTGCATGAA 1752  
Qy 1381 CTGAAATTAATAACATCTTAAGGATTCAGAGGAAACAGAAAGCAGATGCAAGATGGAGGA 1440  
Db 1753 CTGAAATTAATAACATCTTAAGGATTCAGAGGAAACAGAAAGCAGATGCAAGATGGAGGA 1812  
Qy 1441 CAGAAAGGAGCCCTGGGACATTTAAAAAATAAAAAATGAAAAAACCAGAACCCATT 1500  
Db 1813 CAGAAAGGAGCCCTGGGACATTTAAAAAATAAAAAATGAAAAAACCAGAACCCATT 1872  
Qy 1501 TCTCAGGGCACTTTCCAGAAATTCCTCATATTTGTGGCTGGGATCAAGCTGCAGCTTG 1560  
Db 1873 TCTCAGGGCACTTTCCAGAAATTCCTCATATTTGTGGCTGGGATCAAGCTGCAGCTTG 1932  
Qy 1561 AGGAAAGCACAAGAAAGAAAGAAAGATCTGTGTGAAAGCTCAAGTGGCAGCGACCTTG 1620  
Db 1933 AGGAAAGCACAAGAAAGAAAGAAAGATCTGTGTGAAAGCTCAAGTGGCAGCGACCTTG 1992  
Qy 1621 ACTCCACTGAGAACTGCTCAGAAAGTGGGATCAACAATTGGCTGAAAGCCCTGCTC 1680  
Db 1993 ACTCCACTGAGAACTGCTCAGAAAGTGGGATCAACAATTGGCTGAAAGCCCTGCTC 2052  
Qy 1681 ACTCTAGGGCACTGACCTGCTCTTGTGCTTAACCAAGAGCTAAGGCTATAGCAAT 1740  
Db 2053 ACTCTAGGGCACTGACCTGCTCTTGTGCTTAACCAAGAGCTAAGGCTATAGCAAT 2112  
Qy 1741 GGTTCCTTAGAAACAGTAAACAGTTTCTAGGAGTGGCCTTGGCTGGGGATGACA 1800

Db 2113 GGTTCCTTAGAAACAGTAAACAGTTTCTAGGAGTGGCCTTGGCTGGGGATGACA 2172  
Qy 1801 GTGTGGAGCTGTGGGGTACTGAGAAAGACACATTCCTTGAAGGTCTTAAGAGCCAG 1860  
Db 2173 GTGTGGAGCTGTGGGGTACTGAGAAAGACACATTCCTTGAAGGTCTTAAGAGCCAG 2232  
Qy 1861 GT 1920  
Db 2233 GT 2292  
Qy 1921 AGAACTCTCAGGCGTAATGAAAAATCAGCTCAAAATGAGATCAGAGCCGCCAGGGTCC 1980  
Db 2293 AGAACTCTCAGGCGTAATGAAAAATCAGCTCAAAATGAGATCAGAGCCGCCAGGGTCC 2352  
Qy 1981 ACCCAGAGACATACAGAGCTCTGAAAGACATAGCACCAAGCGAGCCCTTCAGATT 2040  
Db 2353 ACCCAGAGACATACAGAGCTCTGAAAGACATAGCACCAAGCGAGCCCTTCAGATT 2412  
Qy 2041 CCCCACCTGTCATCGGAGATGCTCAGAGTGTGAGGCACTTAAGGGCTCCAGCA 2100  
Db 2413 CCCCACCTGTCATCGGAGATGCTCAGAGTGTGAGGCACTTAAGGGCTCCAGCA 2472  
Qy 2101 TGGCATATCCATGCCACGGT 2160  
Db 2473 TGGCATATCCATGCCACGGT 2532  
Qy 2161 GGGATTCAGAGCTGAGGTGGAGTGAAGATGTTTCCAGAGAACAGTTTCACTCTAAG 2220  
Db 2533 GGGATTCAGAGCTGAGGTGGAGTGAAGATGTTTCCAGAGAACAGTTTCACTCTAAG 2592  
Qy 2221 GTCCGAAATGTTCCCTTTAACCCTGAGTGGAGTGAAGGGGTATACCAAGATTTT 2280  
Db 2593 GTCCGAAATGTTCCCTTTAACCCTGAGTGGAGTGAAGGGGTATACCAAGATTTT 2652  
Qy 2281 TCCCTACAGCTGATGAGCAATGATGCTTGAATAATTCAGACACCTCCCTGAACT 2340  
Db 2653 TCCCTACAGCTGATGAGCAATGATGCTTGAATAATTCAGACACCTCCCTGAACT 2712  
Qy 2341 CATTTGTCAGAGAGAGGGCCCATCTGTGTCTGTAAACATGCTTTCAATGATCACCTTC 2400  
Db 2713 CATTTGTCAGAGAGAGGGCCCATCTGTGTCTGTAAACATGCTTTCAATGATCACCTTC 2772  
Qy 2401 TTGTCATGTTCCAGCTGCTTCCCAACCTGGAAGGCCGTTCCTTGAAGCAAGTCTCC 2460  
Db 2773 TTGTCATGTTCCAGCTGCTTCCCAACCTGGAAGGCCGTTCCTTGAAGCAAGTCTCC 2832  
Qy 2461 TCAAGGCTTGAAGAACTTCCACAGGTCACTCCTCAATTGAGGCTCTGATCACTCCA 2520  
Db 2833 TCAAGGCTTGAAGAACTTCCACAGGTCACTCCTCAATTGAGGCTCTGATCACTCCA 2892  
Qy 2521 TCCCTCTCTACCCCTCCCTCCCAACCTCAATGATTAATTTGCTTTGATGCTTAG 2580  
Db 2893 TCCCTCTCTACCCCTCCCTCCCAACCTCAATGATTAATTTGCTTTGATGCTTAG 2952  
Qy 2581 CATTCACATTTTGAATGATGATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640  
Db 2953 CATTCACATTTTGAATGATGATTTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3012  
Qy 2641 GTAAACCTTGGTGGTGGGGGCAATTCCTTGAACCTCTCTGTATCCCAAGATATCT 2700  
Db 3013 GTAAACCTTGGTGGTGGGGGCAATTCCTTGAACCTCTCTGTATCCCAAGATATCT 3072  
Qy 2701 GTAACAGTGCAGGCAC-CAGAAAGTGAATCAAT 2734  
Db 3073 GTAACAGTGCAGGCACACAGTAGTGAATCAAT 3107

RESULT 4  
ABZ71540  
ID ABZ71540 standard; DNA; 3126 BP.  
XX  
AC ABZ71540;  
XX





CC a pharmaceutical composition for diagnosing or treating diabetes or  
CC conditions related to diabetes. The present sequence is that of the human  
CC immunoglobulin Fc portion used to generate fusion proteins, increasing  
CC the stability of the fused protein as compared to the secreted protein  
CC only. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPD at ftp.wipo.int/pub/published\_pcl\_sequences.

XX  
Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;

Query Match 99.0%; Score 2715; DB 9; Length 3126;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2729; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 AGAAGTCAGCTGGCAGAGAGACTGTGAATGAGGGAATTAGAGTGTTCAGAGAGAGA 60  
DB 373 AGAAGTCAGCTGGCAGAGAGACTGTGAATGAGGGAATTAGAGTGTTCAGAGAGAGA 432  
QY 61 GCTTCAGCTGAGAGACAGAGAGAGAGCTCCCTGAAGAGCTTCTAAGAGAGTCTGCCAT 120  
DB 433 GCTTCAGCTGAGAGACAGAGAGAGAGCTCCCTGAAGAGCTTCTAAGAGAGTCTGCCAT 492  
QY 121 GGCCTCTCTTGGCCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 180  
DB 493 GGCCTCTCTTGGCCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 552  
QY 181 ACTGCTTGCATGTCTGTCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 240  
DB 553 ACTGCTTGCATGTCTGTCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 612  
QY 241 GACAGCAGTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGACAGAGCAT 300  
DB 613 GACAGCAGTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGACAGAGCAT 672  
QY 301 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTTCCCGCTGACATCCAGGCTGCCA 360  
DB 673 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTTCCCGCTGACATCCAGGCTGCCA 732  
QY 361 GGCCTCTCTTGGCCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 420  
DB 733 GGCCTCTCTTGGCCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGCTTTTGGGAC 792  
QY 421 CATGAGATGACAGTCTTCTGCCAGAGATCCCGAGCCAGAGACAGAGTGGCGGTAGCAG 480  
DB 793 CATGAGATGACAGTCTTCTGCCAGAGATCCCGAGCCAGAGACAGAGTGGCGGTAGCAG 852  
QY 481 TGAAGTCTTCTTCACTCTTGAAGGCTCTGGAGTTCAATCTCTGTTGCTTGAATCTTCA 540  
DB 853 TGAAGTCTTCTTCACTCTTGAAGGCTCTGGAGTTCAATCTCTGTTGCTTGAATCTTCA 912  
QY 541 TGGGATCTTCAAGGAGCTTCTTCACTCACTGAGTCCAGAGCATGAAATTTGAGTTGG 600  
DB 913 TGGGATCTTCAAGGAGCTTCTTCACTCACTGAGTCCAGAGCATGAAATTTGAGTTGG 972  
QY 601 AGAGGCTCTTCACTTGAAGGATTTCTGCTCCCTGTTCCCTGATAGCTGGAATCATCT 660  
DB 973 AGAGGCTCTTCACTTGAAGGATTTCTGCTCCCTGTTCTCCCTGATAGCTGGAATCATCT 1032  
QY 661 CTGCTTCTCTGCTCATCTCCAGAGAAATGCTCCCACTACTACGATCTCAAGGCCA 720  
DB 1033 CTGCTTCTCTGCTCATCTCCAGAGAAATGCTCCCACTACTACGATCTCAAGGCCA 1092  
QY 721 ACCTCTTTCAGACAGAGAGCTTCTCAAGGCTGTCAACTTCCAAAGTCAAGAGTGAATT 780  
DB 1093 ACCTCTTTCAGACAGAGAGCTTCTCAAGGCTGTCAACTTCCAAAGTCAAGAGTGAATT 1152  
QY 781 CAATCTCTAAGAGCTTCAAGGCTGTCAACTTCCAAAGTCAAGAGTGAATT 840  
DB 1153 CAATCTCTAAGAGCTTCAAGGCTGTCAACTTCCAAAGTCAAGAGTGAATT 1212  
QY 841 TGGGCTCTGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
DB 1213 TGGGCTCTGAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272

QY 901 GATCTGTGACAGAGAGTGTGCTGAGATAGACTGACTTTTGGCATTGATGAGCAAG 960  
DB 1273 GATCTGTGACAGAGAGTGTGCTGAGATAGACTGACTTTTGGCATTGATGAGCAAG 1332  
QY 961 GCAGAAATGGGGCTAGTGTAAACAGATCAGAGTGAATTTGCCAGAGATGCTGCCATGC 1020  
DB 1333 GCAGAAATGGGGCTAGTGTAAACAGATCAGAGTGAATTTGCCAGAGATGCTGCCATGC 1392  
QY 1021 GAGCTTCTGTTTCTGACCTTGTGCTCCCTGCTCCCTGAAGTCCCAAGCTCAACTT 1080  
DB 1393 GAGCTTCTGTTTCTGACCTTGTGCTCCCTGCTCCCTGAAGTCCCAAGCTCAACTT 1452  
QY 1081 GAAACCCCAATCCCTTAAAGCAGAGACTCAGAGATCCCTTGTGCTCTGTTTAACTGGG 1140  
DB 1453 GAAACCCCAATCCCTTAAAGCAGAGACTCAGAGATCCCTTGTGCTCTGTTTAACTGGG 1512  
QY 1141 ACTCATCTCCCAAGCCCACTAATCAGATCCCACTGAAGCTCTGTGTATCAAGAGCC 1200  
DB 1513 ACTCATCTCCCAAGCCCACTAATCAGATCCCACTGAAGCTCTGTGTATCAAGAGCC 1572  
QY 1201 TCTCTGTGAGTGTGCTCTTAACTGCTGTGGGATGGGAGAGAGAGAGAGAGAGAGAG 1260  
DB 1573 TCTCTGTGAGTGTGCTCTTAACTGCTGTGGGATGGGAGAGAGAGAGAGAGAGAGAG 1632  
QY 1261 TTTTGTGGGATGTGCTTAACTGCTTCAAGCTTCCCTCAAGAGAACTGATTTGGGCC 1320  
DB 1633 TTTTGTGGGATGTGCTTAACTGCTTCAAGCTTCCCTCAAGAGAACTGATTTGGGCC 1692  
QY 1321 TGAACCTCCATCCCACTCTTGTATGACTCAAGTGTCCAGATTAATTTGTGATGAA 1380  
DB 1693 TGAACCTCCATCCCACTCTTGTATGACTCAAGTGTCCAGATTAATTTGTGATGAA 1752  
QY 1381 CTGAATTAAGCACTCTAAGGATTCAGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
DB 1753 CTGAATTAAGCACTCTAAGGATTCAGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1812  
QY 1441 CAG 1500  
DB 1813 CAG 1872  
QY 1501 TCTCAGGAGCACTTTCAGAAATCTCTCATATTTTGGGCTGGGATCAAGCTGACCTTG 1560  
DB 1873 TCTCAGGAGCACTTTCAGAAATCTCTCATATTTTGGGCTGGGATCAAGCTGACCTTG 1932  
QY 1561 AGGAAAGCAG 1620  
DB 1933 AGGAAAGCAG 1992  
QY 1621 ACTCACTGAG 1680  
DB 1993 ACTCACTGAG 2052  
QY 1681 ACTCACTGAG 1740  
DB 2053 ACTCACTGAG 2112  
QY 1741 GGTTCCTTGAAGACAGTAAACAGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
DB 2113 GGTTCCTTGAAGACAGTAAACAGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2172  
QY 1801 GTGTGGAG 1860  
DB 2173 GTGTGGAG 2232  
QY 1861 GTGTGGAG 1920  
DB 2233 GTGTGGAG 2292  
QY 1921 AGAAACTCTTCAAGGCTTAATGAGAAATCAAGTCAATGAGATCAAGGCTCCCAAGGCTC 1980  
DB 2293 AGAAACTCTTCAAGGCTTAATGAGAAATCAAGTCAATGAGATCAAGGCTCCCAAGGCTC 2352











Accession	Contig	Position	Sequence	Length
QY	901		GGATCGGTGTCAGAAAGTGTCTGTAGGTAATACATGCTTTTGGCAATTGGAGCAAG	960
Db	859		GGATCGGTGTCAGAAAGTGTCTGTAGGTAATACATGCTTTTGGCAATTGGAGCAAG	800
QY	961		GCAGAAATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATGCTGCCATGC	1020
Db	799		GCAGAAATGGGGGCTAGTGTAAACAGCATGCAAGTTGAATTGCCAAGATGCTGCCATGC	740
QY	1021		CAGCCTTTCTGTCTTCTCACTTGTCTCTCCCTGTAGTCCCAACCTTCACTT	1080
Db	739		CAGCCTTTCTGTCTTCTCACTTGTCTCTCCCTGTAGTCCCAACCTTCACTT	680
QY	1081		GAAACCCCATTCCTTTAAGCCAGAGCTCAGAGATCCCTTGGCCCTGTGTTA - CCGT	1138
Db	679		GAAACCCCATTCCTTTAAGCCAGAGCTCAGAGATCCCTTGGCCCTGTGTTA	620
QY	1139		GGACTTC - -ATCCCCAACCACCTAATCACATCCACTGACTGACCTCTGTATCAA	1195
Db	619		GGACTTCATCCCCAACCACCTAATCACATCCACTGACTGACCTCTGTATCAA	560
QY	1196		GACCCTCTCTGTGCTGAGTGTGGCTTTAGCTCATGCTGAGGATGGGAAAGAGAGCA	1255
Db	559		GACCCTCTCTGTGCTGAGTGTGGCTTTAGCTCATGCTGAGGATGGGAAAGAGAGCA	500
QY	1256		GTGGCTTTTGTGGGATGTCTTAACTTAACCTTCTCAACCTTCCCTCCAAAGACTGAT	1315
Db	499		GTGGCTTTTGTGGGATGTCTTAACTTAACCTTCTCAACCTTCCCTCCAAAGACTGAT	440
QY	1316		GGCCCTGGACCTCATCCCACTCTGTGTATGACTCCACAGTGTCCAGACTAATTGTGC	1375
Db	439		GGCCCTGGACCTCATCCCACTCTGTGTATGACTCCACAGTGTCCAGACTAATTGTGC	380
QY	1376		ATGAACCTGAAATPAAACCATCTTACGGTATCCAGGGAACAGAAACAGATGCAAGATGG	1435
Db	379		ATGAACCTGAAATPAAACCATCTTACGGTATCCAGGGAACAGAAACAGATGCAAGATGG	320
QY	1436		GAGGACAGAAAGGACGCTGTGGACATTTAAAAAATAAAAATGAAAAAACCAGAAC	1495
Db	319		GAGGACAGAAAGGACGCTGTGGACATTTAAAAAATAAAAATGAAAAAACCAGAAC	260
QY	1496		CCATTTCTCAGGGGCACTTTCAGAAATTCCTCATATTGTGGGGCTGGATCAAGCTGCA	1555
Db	259		CCATTTCTCAGGGGCACTTTCAGAAATTCCTCATATTGTGGGGCTGGATCAAGCTGCA	200
QY	1556		GCTTGAGAAAGCACAAGAAAGAAAGAAAGATCTGTGTGAAGCTCAGGTGGACGCGA	1615
Db	199		GCTTGAGAAAGCACAAGAAAGAAAGAAAGATCTGTGTGAAGCTCAGGTGGACGCGA	140
QY	1616		CTTGACTCTCACTGAGAACTGCTCTCAGAAAGTGGCATCAACTTTGGCTGAAGCCCT	1675
Db	139		CTTGACTCTCACTGAGAACTGCTCTCAGAAAGTGGCATCAACTTTGGCTGAAGCCCT	80
QY	1676		GCTTCACCTTAGGGGACCTGACCTGGGCTCTTGGCTTAACCAAGGCTAAGGGCTATAG	1735
Db	79		GCTTCACCTTAGGGGACCTGACCTGGGCTCTTGGCTTAACCAAGGCTAAGGGCTATAG	20
QY	1736		ACAATGTTTCTCTTAGGA 1753	
Db	19		ACAATGATTCTTAGGA 2	
RESULT 8				
ADE09922/c				
ID ADE09922 standard; DNA; 1761 BP.				
XX ADE09922;				
AC ADE09922;				
DT 29-JAN-2004 (first entry)				
XX Novel DNA-related contig nucleotide sequence #644.				
DE novel gene; novel protein; tissue marker; molecular weight marker;				
KM chromosome marker; genetic disorder; contig; de.				

XX		Unidentified.	
XX			
FN	W02003054152-A2.		
XX			
PD	03-JUL-2003.		
XX			
PE	10-DEC-2002; 2002WO-US039555.		
XX			
PR	10-DEC-2001; 2001US-0339739P.		
PR	11-DEC-2001; 2001US-0339453P.		
PR	14-MAR-2002; 2002US-0365091P.		
PR	14-MAR-2002; 2002US-0365384P.		
PR	12-APR-2002; 2002US-0372381P.		
PR	12-APR-2002; 2002US-0372615P.		
PR	22-APR-2002; 2002US-00128558.		
PR	24-APR-2002; 2002US-0376045P.		
PA	(HYSB-) HYSBQ INC.		
XX			
P1	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QX, Wang J;		
P1	Ghosh M, Xue AU, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;		
P1	Ma Y, Wang D, Chen R, Xu C, Boyle BU,		
DR	WPI; 2003-569235/53.		
PT	New polynucleotides, useful for expressing recombinant proteins for		
PT	analyses, characterization or therapeutic use, or as markers for tissues		
PT	in which the corresponding protein is preferentially expressed.		
PS	Disclosure; SEQ ID NO 2466; 1177bp; English.		
XX			
CC	The invention comprises the amino acid and coding sequences of novel		
CC	proteins. The DNA and protein sequences of the invention are useful as:		
CC	markers for tissues in which the corresponding protein is preferentially		
CC	expressed; as molecular weight markers on gels; as chromosome markers or		
CC	tags; to identify chromosomes or to map related gene positions; and to		
CC	compare with endogenous DNA sequences in patients to identify potential		
CC	genetic disorders. The present DNA sequence was used in the		
CC	exemplification of the invention.		
SQ	Sequence 1761 BP; 407 A; 446 C; 478 G; 430 T; 0 U; 0 Other;		
	Query Match 62.6%; Score 1716.8; DB 10; Length 1761;		
	Best Local Similarity 99.3%; Pred. No. 0;		
	Matches 1746; Conservative 0; Mismatches 7; Indels 5; Gaps 2.		
QY	1 AGAAGTCAGCCTGGCAGAGAACAATCTGTAAGAAAGAGGATTAGAGGTCTCAAGAGACAGA 60		
Db	1759 AGAAGTCAGCCTGGCAGAGAACAATCTGTAAGAAAGAGGATTAGAGGTCTCAAGAGACAGA 1700		
QY	61 GCTTCAGCGCTGAAGACAAAGGAGAGTCCCTGAAGACGCTTCTACTGAGAGCTTGCCAT 120		
Db	1699 GCTTCAGCGCTGAAGACAAAGGAGAGTCCCTGAAGAGCTTCTACTGAGAGGTTCGCAT 1640		
QY	121 GGCCCTCTTGAGCCTCCAATCTTGAGGCTACATCTTAGGCCCTTTGAGGCTTTTGGCAC 180		
Db	1639 GGCCCTCTTGAGCCTCCAATCTTGAGGCTACATCTTAGGCCCTTTGAGGCTTTTGGCAC 1580		
QY	181 ACTGTTGGCATGCTGCTCCCAGCTGGAAAAAAGTTCTTAATGCGGTGCGACAGATTGT 240		
Db	1579 ACTGTTGGCATGCTGCTCCCAGCTGGAAAAAAGTTCTTAATGCGGTGCGACAGATTGT 1522		
QY	241 GACAGCAGTTGGCTTCTCAAGAGGCTCTGAGATGGAATGTCACACACAGACAGGAGAT 300		
Db	1519 GACAGCAGTTGGCTTCTCAAGAGGCTCTGAGATGGAATGTCACACACAGACAGGAGAT 1460		
QY	301 CACCAGTGTGACATCTATAGACACCTTTCTGAGGCTGCGCGTGCATCTCAGGCTGCCCA 360		
Db	1459 CACCAGTGTGACATCTATAGACACCTTTCTGAGGCTGCGCGCTGCATCTCAGGCTGCCCA 1400		
QY	361 GGCCATGATGTGTGACATCTCAGTGCAACTCTCCCTTGCGCGCATTAATCTGTGAGTGGG 420		

Db	1399	GGCCATGATGGTGA	CATCCAGTGCAGTCACTCCTCCTGGCCTGCACTTATCTGTGGTGGG	1348
Qy	421	CATGAGATGCA	CAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGTATGCAAG	480
Db	1339	CATGGAATGCA	CAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGTATGCAAG	1280
Qy	481	TGAGATCTTTTTC	CATCCTTGGAGGGCTCCTGGGAATTCAATTCCTGTTGGCTGGAATCTTCA	540
Db	1279	TGAGATCTTTTTC	CATCCTTGGAGGGCTCCTGGGAATTCAATTCCTGTTGGCTGGAATCTTCA	1220
Qy	541	TGGATCTTCA	CGGGAATTCTTCACTCAACACTGGTGCCTGACAGACATGAATTTTGAATTTGG	600
Db	1219	TGGATCTTCA	CGGGAATTCTTCACTCAACACTGGTGCCTGACAGACATGAATTTTGAATTTGG	1166
Qy	601	AGAGGCTCTTTA	CTTGGGCAATTATTTCTTCCTGTTCTTCCTGATAGCTGAATATCACTT	660
Db	1159	AGAGGCTCTTTA	CTTGGGCAATTATTTCTTCCTGTTCTTCCTGATAGCTGAATATCACTT	1100
Qy	661	CTGCTTTTCC	GTGCTATCCCAAGAAATGCGTCCAACTAATACATATGCTTCAAGGCCA	720
Db	1099	CTGCTTTTCC	GTGCTATCCCAAGAAATGCGTCCAACTAATACATATGCTTCAAGGCCA	1040
Qy	721	AACCTTTGCA	CAAGAGCTCTCCAAAGGCTGTGTCAACCTCCCAAATGCTCAAGATGATTT	780
Db	1039	AACCTTTGCA	CAAGAGCTCTCCAAAGGCTGTGTCAACCTCCCAAATGCTCAAGATGATTT	980
Qy	781	CAATTCTTCA	CAGCTGACAGGGTATGTGTGAAGAACAGGGGCCACAGAGCTGGGGGGTGGC	840
Db	979	CAATTCTTCA	CAGCTGACAGGGTATGTGTGAAGAACAGGGGCCACAGAGCTGGGGGGTGGC	920
Qy	841	TGGGCTGTG	AAAAACAGTGAACAGCACCCGAGGGGCCACAGGTGAGGGAACATACCACT	900
Db	919	TGGGCTGTG	AAAAACAGTGAACAGCACCCGAGGGGCCACAGGTGAGGGAACATACCACT	860
Qy	901	GGATCTGTG	CAGAAAGTGTCTGTGAGATAGACTGACTTTGGCCATTGGATTTGAGCAAG	960
Db	859	GGATCTGTG	CAGAAAGTGTCTGTGAGATAGACTGACTTTGGCCATTGGATTTGAGCAAG	800
Qy	961	GCAGAAATGG	GGGGCTAGTGTGAACAGCATGACAGTGAATTTGCCAAGATGCTGCCCATGC	1020
Db	799	GCAGAAATGG	GGGGCTAGTGTGAACAGCATGACAGTGAATTTGCCAAGATGCTGCCCATGC	740
Qy	1021	CAGCCTTCTG	TTTTCCTCAACCTTGCTGCTCCCTGCGCTAAGTCCCAACCTTCAACTT	1080
Db	739	CAGCCTTCTG	TTTTCCTCAACCTTGCTGCTCCCTGCGCTAAGTCCCAACCTTCAACTT	680
Qy	1081	GAAGCCCATTT	CCCTTAAAGCAGGACTCAGAGATCCCTTTGGCCCTCTGGTTTA--CCTG	1138
Db	679	GAAGCCCATTT	CCCTTAAAGCAGGACTCAGAGATCCCTTTGGCCCTCTGGTTTAACCTTG	620
Qy	1139	GGACTGCC--	ATCCCCAAACCCTATATCAGATCCCATGACTGACTGACTCTGTGATCMA	1195
Db	619	GGACTGCCAT	CCCCCAAAACCCCACTAATCACAATCCCACTGACTGACCTCTGTATCMA	560
Qy	1196	GACCTCTCT	TGTGCTGAGTTGGCTCTTACTCATTTGCTGGGGAATGGGAAGGAAAGCA	1255
Db	559	GACCTCTCT	TGTGCTGAGTTGGCTCTTACTCATTTGCTGGGGAATGGGAAGGAAAGCA	500
Qy	1256	GTGCTTTTGG	GAGCATGTCTAAACCTAATTCAAGCTTCCCTCCAAAGAACTGATTT	1315
Db	499	GTGCTTTTGG	GAGCATGTCTCTTAACCTAATTCTCAAGCTTCCCTCCAAAGAACTGATTT	440
Qy	1316	GGCCTTGAAC	CTTCATCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTTGTGC	1375
Db	439	GGCCTTGAAC	CTTCATCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTTGTGC	380
Qy	1376	ATGAATCTGA	ATAAATCAATCTTACGGTATCCAGGAAACAGAAACAGATGCAAGATGG	1435
Db	379	ATGAATCTGA	ATAAATCAATCTTACGGTATCCAGGAAACAGAAACAGATGCAAGATGG	320
Qy	1436	GAGACACGAA	AGGAGCTGTGGGACATTTTAAAAAATGAAAAAATGAAAAAATGAAAAAATG	1495
Db	319	GAGACACGAA	AGGAGCTGTGGGACATTTTAAAAAATGAAAAAATGAAAAAATGAAAAAATG	260

OY	1456	CCATTTCCTCAGGGGCACTTTCAGAAATCTCATATTTGGGCTGGGATCAAGCTGCA	1555
Db	259	CCATTTCCTCAGGGGCACTTTCAGAAATCTCATATTTGGGCTGGGATCAAGCTGCA	200
OY	1556	GCTTGAGGAAGCAACAAGAAAAGAAAGATCTGTGGAAAGCTCAAGTGGCAGCGGA	1615
Db	199	GCTTGAGGAAGCAACAAGAAAAGAAAGATCTGTGGAAAGCTCAAGTGGCAGCGGA	140
OY	1616	CTCTGACCTCCACCTAGAAACCTGCTCAGAAAGCTGCATCAACTTTGGCTGAAGCCCT	1675
Db	139	CTCTGACCTCCACCTAGAAACCTGCTCAGAAAGCTGCATCAACTTTGGCTGAAGCCCT	80
OY	1676	GCCCTCACTCTAGGGGCACTTGACCTTGAGCTCTTGGCTTAAACCAAGGCTAAGGCTTAG	1735
Db	79	GCCCTCACTCTAGGGGCACTTGACCTTGAGCTCTTGGCTTAAACCAAGGCTAAGGCTTAG	20
OY	1736	ACAAATGGTTTCCTTAGGA 1753	
Db	19	ACAAATGAGTTCCTTAGGA 2	
RESULT 9			
ID	ABV89278	standard; cDNA; 1918 BP.	
AC	ABV89278;		
DT	13-DEC-2002	(first entry)	
DE	Human colon cancer related cDNA SEQ ID NO 2589.		
XX	Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene;		
KW	ss.		
XX	Homo sapiens.		
PN	MO200258534-A2.		
PD	01-AUG-2002.		
PF	16-NOV-2001; 2001WO-US043704.		
PR	20-NOV-2000; 2000US-0252222P.		
PR	06-FEB-2001; 2001US-0267011P.		
PR	28-MAR-2001; 2001US-0279670P.		
BR	10-JUL-2001; 2001US-0304037P.		
XX	(CORI-) CORIXA CORP.		
PI	Stolk JA, Xu J, Chenault RA, Meagher MJ, Secret H, King GB;		
XX	WPI: 2002-608400/65.		
DR	P-PSDB; ABP67991.		
PT	New isolated tumor colon polynucleotide and polypeptide, useful for the		
XX	diagnosis, prevention and/or treatment of cancer, in particular colon		
XX	cancer.		
PS	Claim 1; SEQ ID NO 2589; 266pp + Sequence Listing; English.		
XX			
CC	The invention relates to a human colon tumour expressed polynucleotide		
CC	(I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of		
CC	2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)		
CC	complements of (i); (iii) at least 20 contiguous residues of (i); (iv)		
CC	sequences that hybridize to (i), under moderately stringent conditions;		
CC	(v) sequences having at least 75% or 90% identity to (i); or (vi)		
CC	degenerate variants of (i). The compositions and methods of the present		
CC	invention are useful for the diagnosis, prevention and/or treatment of		
CC	cancer, particularly colon cancer. (I) can be used in gene therapy and		
CC	(I) and (II) are useful in pharmaceutical compositions such as vaccines.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WPI		

CC RESULT 9  
 AC ABV893278  
 ID ABV893278 standard; cDNA; 1918 BP.  
 XX  
 AC ABV89278;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Human colon cancer related cDNA SEQ ID NO 2589.  
 XX  
 KM Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene;  
 KW 85.  
 OS Homo sapiens.  
 PM WO200258534-A2.  
 PN  
 XX  
 PD 01-AUG-2002.  
 PF 16-NOV-2001; 2001WO-US043704.  
 PR 20-NOV-2000; 2000US-0252222P.  
 PR 06-FEB-2001; 2001US-0267011P.  
 PR 28-MAR-2001; 2001US-0279670P.  
 PR 10-JUL-2001; 2001US-0304037P.  
 XX  
 PA (CORI-) CORITA CORP.  
 XX  
 PI Stolk JA, Xu J, Chénault RA, Meagher WJ, Secret H, King GE;  
 DR MPI; 2002-608400/65.  
 DR P-PADB; ABP67991.  
 XX  
 PT New isolated tumor colon polynucleotide and polypeptide, useful for the  
 FT diagnosis, prevention and/or treatment of cancer, in particular colon  
 TT cancer.  
 XX  
 PS Claim 1; SEQ ID NO 2589; 26kbp + Sequence Listing; English.  
 XX  
 The invention relates to a human colon tumour expressed polynucleotide  
 CC (I) encoding a polypeptide (II), ABP67991-ABP67996) comprising: (i) any of  
 CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)  
 CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)  
 CC sequences that hybridize to (i), under moderately stringent conditions;  
 CC (v) sequences having at least 75% or 90% identity to (i); or (vi)  
 CC degenerate variants of (i). The compositions and methods of the present  
 CC invention are useful for the diagnosis, prevention and/or treatment of  
 CC cancer, particularly colon cancer. (I) can be used in gene therapy and  
 CC (I) and (II) are useful in pharmaceutical compositions such as vaccines.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO



PS Claim 5; Page 11-12 (Disclosure); 42bp; Chinese.  
 CC The present sequence encodes human SP82 protein, which has cancer-  
 CC suppressing activity. The present invention also describes a method for  
 CC the preparation of the protein by recombination, and the application of  
 CC the protein in treating diseases such as cancer

SQ Sequence 1918 BP; 486 A; 525 C; 473 G; 434 T; 0 U; 0 Other;

Query Match 54.1%; Score 1482.8; DB 6; Length 1918;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1487; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTGAGGTGTTCAAGAGCAAGA 60  
 DB AGAAGTCAGCTGGCAGAGAGAGACTCTGAATGAGGATTGAGGTGTTCAAGAGCAAGA 461  
 QY 61 GCTTCAAGCTGAG 120  
 DB GCTTCAAGCTGAG 521  
 QY 121 GGCCTCTCTGAGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 180  
 DB GGCCTCTCTGAGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 581  
 QY 522 GGCCTCTCTGAGCTCCCACTTGTGGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 581  
 DB 181 ACTGTTGTCATGCTGCTGCTCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240  
 DB 582 ACTGTTGTCATGCTGCTGCTCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 641  
 QY 241 GAG 300  
 DB GAG 701  
 QY 301 CACCAAGTGTGATCTATAGCAAGCTTCTGGGCTGCGGCTGAGCAATCCAGAGCTGCCA 360  
 DB CACCAAGTGTGATCTATAGCAAGCTTCTGGGCTGCGGCTGAGCAATCCAGAGCTGCCA 761  
 QY 702 CACCAAGTGTGATCTATAGCAAGCTTCTGGGCTGCGGCTGAGCAATCCAGAGCTGCCA 761  
 DB 361 GGCATGATGTGATCATCATGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 DB 762 GGCATGATGTGATCATCATGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 821  
 QY 421 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 DB CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 881  
 QY 882 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 881  
 DB 481 TGGAGTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 540  
 DB 882 TGGAGTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 941  
 QY 541 TGGAGTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 600  
 DB 942 TGGAGTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 1001  
 QY 601 AGAGGCTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 660  
 DB 1002 AGAGGCTCTTTTTCATCTTGGAGGCTCTGAGATTCATCTGTTGCTGAGATCTTCA 1061  
 QY 661 CTGCTTTTCTGCTGATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGAGCCCA 720  
 DB 1062 CTGCTTTTCTGCTGATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGAGCCCA 1121  
 QY 721 ACCTCTTTCAGAGAGAGCTCTCCAGAGCTGCTGCTCAACCTCCAAAGTCAAGATGAT 780  
 DB 1122 ACCTCTTTCAGAGAGAGCTCTCCAGAGCTGCTGCTCAACCTCCAAAGTCAAGATGAT 1181  
 QY 781 CAATTTCTTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 DB 1182 CAATTTCTTACAGCTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1241  
 QY 841 TGGGCTGTGAG 900  
 DB 1242 TGGGCTGTGAG 1301

QY 901 GATTCGTGAG 960  
 DB 1302 GATTCGTGAG 1361  
 QY 961 GCAAGATGAG 1020  
 DB 1362 GCAAGATGAG 1421  
 QY 1021 CAGCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 DB 1422 CAGCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481  
 QY 1081 GAAACCCCATTCCTTTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 DB 1482 GAAACCCCATTCCTTTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1541  
 QY 1141 ACTCCATTCCTCCAAAGCCATCATCATCATCATCATCATCATCATCATCATCATCAT 1200  
 DB 1542 ACTCCATTCCTCCAAAGCCATCATCATCATCATCATCATCATCATCATCATCATCAT 1601  
 QY 1201 TCTCTGAGCTGAG 1260  
 DB 1602 TCTCTGAGCTGAG 1661  
 QY 1261 TTTTGTGGGATGCTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1320  
 DB 1662 TTTTGTGGGATGCTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1721  
 QY 1321 TGGACCTCCATCCCATCTGTTTATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
 DB 1722 TGGACCTCCATCCCATCTGTTTATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1781  
 QY 1381 CTGAAATTAACCATCTCTAAGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 DB 1782 CTGAAATTAACCATCTCTAAGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1841  
 QY 1441 CAGGAGGAG 1494  
 DB 1842 CAGGAGGAG 1895

RESULT 11  
 AAA37060  
 ID AAA37060 standard; cDNA; 1475 BP.  
 XX  
 AC AAA37060;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Human PRL1356 (UN0705) cDNA sequence SEQ ID NO:133.  
 XX  
 KM Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.  
 OS Homo sapiens.  
 XX  
 PN MO200012708-A2.  
 PD 09-MAR-2000.  
 XX  
 PF 01-SEP-1999; 99MO-US020111.  
 XX  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.  
 PR 09-SEP-1998; 98US-0099596P.  
 PR 09-SEP-1998; 98US-0099602P.  
 PR 09-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0097741P.  
PR 10-SEP-1998; 98US-009754P.  
PR 10-SEP-1998; 98US-009763P.  
PR 10-SEP-1998; 98US-009792P.  
PR 10-SEP-1998; 98US-009808P.  
PR 10-SEP-1998; 98US-009812P.  
PR 10-SEP-1998; 98US-009815P.  
PR 10-SEP-1998; 98US-009816P.  
PR 15-SEP-1998; 98US-0100385P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101473P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-0103314P.  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103395P.  
PR 07-OCT-1998; 98US-0103396P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103637P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.

PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106565P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 18-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.

(GETH ) GENENTECH INC.

XX Baker K, Goddard A, Gurney AU, Smith V, Watanabe CK, Wood WT;

XX WPI; 2000-237871/20.

XX P-PSDB; AAY9378.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
PT PRO polypeptides, useful for screening of potential peptide or small  
PT molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 2; Fig 77; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding them have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR  
CC primers and hybridisation probes used in the isolation of the PRO  
XX polypeptides from the present invention

SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Query Match 53.7%; Score 1472; DB 3; Length 1475;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATATGAGGATTTAGAGCTTCAAGAGCAGA 60  
|||  
Db 4 AGAAGTCAGCTGGCAGAGAGACTCTGAATATGAGGATTTAGAGCTTCAAGAGCAGA 63  
61 GCTTCAGCTGAGAGCAGAGGAGCAGTCCCTGAAGAGCTTCTAAGAGAGTCTCCAT 120

Db 64 GCTTCAGCCCTGAAAGACAAAGGAGAGCACTCCCTGAAAGAGCTTCTACTAGAGGCTGTCAT 123  
 Qy 121 GGGCTCTTGGGCTCCAACTGTGGGCTACATCTTAGAGGCTTCTGGGGCTTTTGGGAC 180  
 Db 124 GGGCTCTTGGGCTCCAACTGTGGGCTACATCTTAGAGGCTTCTGGGGCTTTTGGGAC 183  
 Qy 181 ACTGTTGCAATGCTGCTCCAGCTGGAACAAAGTTCTTATGTGCGGTCCAGCATGT 240  
 Db 184 ACTGTTGCAATGCTGCTCCAGCTGGAACAAAGTTCTTATGTGCGGTCCAGCATGT 243  
 Qy 241 GACAGCATTTGGCTTCTCCAAAGGCTCTGATGGAATGTGCCACACACAGCAGGAT 300  
 Db 244 GACAGCATTTGGCTTCTCCAAAGGCTCTGATGGAATGTGCCACACACAGCAGGAT 303  
 Qy 301 CACCAAGTGAATCTATAGCAACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 360  
 Db 304 CACCAAGTGAATCTATAGCAACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 363  
 Qy 361 GGGCATGATGATGATCATCATGCAATCTCTCCCTGAGCTGCAATATCTGTGTGG 420  
 Db 364 GGGCATGATGATGATCATCATGCAATCTCTCCCTGAGCTGCAATATCTGTGTGG 423  
 Qy 421 CATGATGATGATGATCATCATGCAATCTCTCCCTGAGCTGCAATATCTGTGTGG 480  
 Db 424 CATGATGATGATGATCATCATGCAATCTCTCCCTGAGCTGCAATATCTGTGTGG 483  
 Qy 481 TGAAGTCTTTTCTATCTGGAAGGCTCTGGAATTCATTCCTGTTGCTGAACTTCA 540  
 Db 484 TGAAGTCTTTTCTATCTGGAAGGCTCTGGAATTCATTCCTGTTGCTGAACTTCA 543  
 Qy 541 TGGGATCTCAAGGACTTCTACTACCACTGTGCTGACAGCATGAAATTTGAGATTGG 600  
 Db 544 TGGGATCTCAAGGACTTCTACTACCACTGTGCTGACAGCATGAAATTTGAGATTGG 603  
 Qy 601 AGAGGCTCTTACTTGGGCAATATTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 660  
 Db 604 AGAGGCTCTTACTTGGGCAATATTTCTTCCCTGTTCTCCCTGATGCTGGAATCATCT 663  
 Qy 661 CTGCTTTTCTGTCATCCAGAAATGCTCCCAATACAGATGCTACCAAGGCCA 720  
 Db 664 CTGCTTTTCTGTCATCCAGAAATGCTCCCAATACAGATGCTACCAAGGCCA 723  
 Qy 721 ACCTCTTGCACAAAGAGCTCTCCAAAGCTGTGTCACTTCCAAAGTCAAGAGTGT 780  
 Db 724 ACCTCTTGCACAAAGAGCTCTCCAAAGCTGTGTCACTTCCAAAGTCAAGAGTGT 783  
 Qy 781 CATTTCTCAAGCTGACAGGCTATGTGTGAAGAACAGGGGCTCAAGCTGGGGGGTGGC 840  
 Db 784 CATTTCTCAAGCTGACAGGCTATGTGTGAAGAACAGGGGCTCAAGCTGGGGGGTGGC 843  
 Qy 841 TGGGCTCTGTAAGAAAGAGTGAAGCAACCCGAGAGGCTCAGAGTGAAGGACATCACT 900  
 Db 844 TGGGCTCTGTAAGAAAGAGTGAAGCAACCCGAGAGGCTCAGAGTGAAGGACATCACT 903  
 Qy 901 GATCTGTGTAAGAGTGTCTGAGAGTACTGACTTTTGGCATTGATGAGCAAG 960  
 Db 904 GATCTGTGTAAGAGTGTCTGAGAGTACTGACTTTTGGCATTGATGAGCAAG 963  
 Qy 961 GCGAATATGGGGCTATGTATACAGATGAGAGTTGAATTGCCAAGATGCTGCCATGC 1020  
 Db 964 GCGAATATGGGGCTATGTATACAGATGAGAGTTGAATTGCCAAGATGCTGCCATGC 1023  
 Qy 1021 CAGCCTTTCTGTTTCTCTACCTTGTGCTCCCTGAGCTTACTAGTCCCAAGCTCACT 1080  
 Db 1024 CAGCCTTTCTGTTTCTCTACCTTGTGCTCCCTGAGCTTACTAGTCCCAAGCTCACT 1083  
 Qy 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGATCCCTTGTGCTTGTATACCTGGG 1140  
 Db 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGATCCCTTGTGCTTGTATACCTGGG 1143  
 Qy 1141 ACTCCATCCCAAAACCATTAATCACTCCCACTGACTGACCTCTGTGATCAAAAGACC 1200

Db 1144 ACTCCATCCCAAAACCATTAATCACTCCCACTGACTGACCTCTGTGATCAAAAGACC 1203  
 Qy 1201 TCTCTGCTGAGTGTGCTCTTACTGATCTGAGGATGGAAGAGACAGTGGC 1260  
 Db 1204 TCTCTGCTGAGTGTGCTCTTACTGATCTGAGGATGGAAGAGACAGTGGC 1263  
 Qy 1261 TTTTGTGGGCAATGCTTAACTTCTTCAAGCTTCCCTCAAAGAACTGATTGGCCC 1320  
 Db 1264 TTTTGTGGGCAATGCTTAACTTCTTCAAGCTTCCCTCAAAGAACTGATTGGCCC 1323  
 Qy 1321 TGGAACTCATCCCACTCTGTATGACTCCCAAGTGTCCAGATCTAATTGTGATGAA 1380  
 Db 1324 TGGAACTCATCCCACTCTGTATGACTCCCAAGTGTCCAGATCTAATTGTGATGAA 1383  
 Qy 1381 CTGAAATTAACCATCTTACGATATCAGGAAACAGAAAGCAGATGAGATGGAGGA 1440  
 Db 1384 CTGAAATTAACCATCTTACGATATCAGGAAACAGAAAGCAGATGAGATGGAGGA 1443  
 Qy 1441 CAGAAAGCAGCTGGGACATTTAAAAATA 1472  
 Db 1444 CAGAAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 12  
 AAF54296  
 ID AAF54296 standard; DNA; 1475 BP.  
 XX  
 AC AAF54296;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE DNA encoding protein of the invention #39.  
 XX  
 KM Secreted; transmembrane; gene therapy; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078961-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 18-FEB-2000; 2000MO-US004342.  
 XX  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99MO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 02-DEC-1999; 99MO-US030095.  
 PR 16-DEC-1999; 99MO-US030095.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000376.  
 XX  
 PA (GENT) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Pan J, Paoni NF, Roy M, Smith V, Stewart TR, Tumas D, Watanabe CK, Williams PM, Wood WT,  
 PI Williams PM, Wood WT,  
 DR WPI; 2001-071395/08.  
 XX  
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX  
 PS Claim 2; Fig 77; 787pp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either





PR 06-JAN-2000; 2000MO-US000277.  
PR 06-JAN-2000; 2000MO-US000376.  
PR 11-FEB-2000; 2000MO-US000365.  
PR 18-FEB-2000; 2000MO-US000431.  
PR 18-FEB-2000; 2000MO-US000432.  
PR 22-FEB-2000; 2000MO-US000414.  
PR 24-FEB-2000; 2000MO-US000414.  
PR 24-FEB-2000; 2000MO-US000504.  
PR 01-MAR-2000; 2000MO-US000501.  
PR 02-MAR-2000; 2000MO-US000584.  
PR 03-MAR-2000; 2000MO-US000584.  
PR 10-MAR-2000; 2000MO-US000584.  
PR 15-MAR-2000; 2000MO-US000584.  
PR 20-MAR-2000; 2000MO-US000584.  
PR 21-MAR-2000; 2000MO-US000584.  
PR 17-MAY-2000; 2000MO-US000584.  
PR 22-MAY-2000; 2000MO-US000584.  
PR 30-MAY-2000; 2000MO-US000584.  
PR 02-JUN-2000; 2000MO-US000584.  
PR 05-JUN-2000; 2000MO-US000584.  
PR 28-JUL-2000; 2000MO-US000584.  
PR 11-AUG-2000; 2000MO-US000584.  
PR 23-AUG-2000; 2000MO-US000584.  
PR 24-AUG-2000; 2000MO-US000584.  
PR 08-NOV-2000; 2000MO-US000584.  
PR 10-NOV-2000; 2000MO-US000584.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Geritsen M, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI: 2001-408261/43.  
DR P-PSDB; AAU12417.  
XX

PT Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.  
XX  
XX Claim 3; Fig 491; 813pp; English.  
XX

CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy  
XX  
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;

Query Match 53.7%; Score 1472; DB 4; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGGCTGGCAGAGAGACTCTGAATGAGGATTAGAGTCTTCAAGAGCAGA 60  
|||||

Db 4 AGAAGTCAGGCTGGCAGAGAGACTCTGAATGAGGATTAGAGTCTTCAAGAGCAGA 63  
QY 61 GCTTACGCTGGAAGACAGAGAGAGCACTCCCTGGAAGACGCTTCTACTGAGAGGTCTGCAT 120  
Db 64 GCTTACGCTGGAAGACAGAGAGAGCACTCCCTGGAAGACGCTTCTACTGAGAGGTCTGCAT 123  
QY 121 GGCCTCTCTTGGGCTTCAACTTGTGGGCTTCACTTCAAGGCTTCTTGGGCTTCTTGGGCTC 180  
Db 124 GGCCTCTCTTGGGCTTCAACTTGTGGGCTTCACTTCAAGGCTTCTTGGGCTTCTTGGGCTC 183  
QY 181 ACTGTTGCAATGCTGCTCCCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 240  
Db 184 ACTGTTGCAATGCTGCTCCCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 243  
QY 241 GACAGAGATGGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG 300  
Db 244 GACAGAGATGGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG 303  
QY 301 CACCCAGTGTGACATCTTATGACACCTTCTGGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG 360  
Db 304 CACCCAGTGTGACATCTTATGACACCTTCTGGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG 363  
QY 361 GGCAGATGATGAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 420  
Db 364 GGCAGATGATGAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 423  
QY 421 CATGAGATGACATGCTTCTGCAAGGATCCGAGCCAGGCAAGACAGAGTGGGCTGACAG 480  
Db 424 CATGAGATGACATGCTTCTGCAAGGATCCGAGCCAGGCAAGACAGAGTGGGCTGACAG 483  
QY 481 TGGAGCTTTTTCATCTCTTGGAGGCTCTGGAGATTCATCTCTGTTGCTGGAATCTTGA 540  
Db 484 TGGAGCTTTTTCATCTCTTGGAGGCTCTGGAGATTCATCTCTGTTGCTGGAATCTTGA 543  
QY 541 TGGAGCTTCTACGAGGATCTTCTACCTCACCTGAGCTGACAGATGAATTTGAGATTGG 600  
Db 544 TGGAGCTTCTACGAGGATCTTCTACCTCACCTGAGCTGACAGATGAATTTGAGATTGG 603  
QY 601 AGAGGCTCTTTCATCTTGGAGGATTTCTTCTGTTCTCTGTTGCTGGAATCTTGA 660  
Db 604 AGAGGCTCTTTCATCTTGGAGGATTTCTTCTGTTCTCTGTTGCTGGAATCTTGA 663  
QY 661 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCCATCTTACAGAGCTTACAGGCCA 720  
Db 664 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCCATCTTACAGAGCTTACAGGCCA 723  
QY 721 ACCTTTGCAAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAG 780  
Db 724 ACCTTTGCAAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAG 783  
QY 781 CATTTCTTACAGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 840  
Db 784 CATTTCTTACAGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 843  
QY 841 TGGGCTTGAAGAAACAGAGGACAGACCCCAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTT 900  
Db 844 TGGGCTTGAAGAAACAGAGGACAGACCCCAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTT 903  
QY 901 GATTCGTCAGAGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 960  
Db 904 GATTCGTCAGAGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 963  
QY 961 GCAGAAATGGGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 1020  
Db 964 GCAGAAATGGGGCTTGAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAG 1023  
QY 1021 CAGCTTTCTGTTTCTTCACTTGTGCTCCCTGCTTCAAGTCCCAAGCTTCAAGCTTCAAGCTT 1080  
Db 1024 CAGCTTTCTGTTTCTTCACTTGTGCTCCCTGCTTCAAGTCCCAAGCTTCAAGCTTCAAGCTT 1083  
QY 1081 GAAACCCATTCCTTCAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTT 1140  
Db 1084 GAAACCCATTCCTTCAAGGATTTGTAAGAACAGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTT 1143

QY 1141 ACTGCATCCCAACCACTAATCATGACGACCTCTGTGATCAAGACCC 1200  
DB 1144 ACTGCATCCCAACCACTAATCATGACGACCTCTGTGATCAAGACCC 1203  
QY 1201 TCTCTGCTGAGTGGCTCTTACCTCATGCTGGGATGGAGAGAGAGTGC 1260  
DB 1204 TCTCTGCTGAGTGGCTCTTACCTCATGCTGGGATGGAGAGAGAGTGC 1263  
QY 1261 TTTTGTGGGATGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1320  
DB 1264 TTTTGTGGGATGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATGGCCC 1323  
QY 1321 TGGAACTGCATCCCACTCTTGTATGATGACGACGATCCAGCTAATTTGGCATGAA 1380  
DB 1324 TGGAACTGCATCCCACTCTTGTATGATGACGACGATCCAGCTAATTTGGCATGAA 1383  
QY 1381 CTGAATATTAACATCTTACGCTATCCAGGAAACAGAGCAGATGCGAGGA 1440  
DB 1384 CTGAATATTAACATCTTACGCTATCCAGGAAACAGAGCAGATGCGAGGA 1443  
QY 1441 CAGGAGGCGCTGGGACATTTAAAAATA 1472  
DB 1444 CAGGAGGCGCTGGGACATTTAAAAATA 1475  
RESULT 14  
AAS15360  
ID AAS15360 standard; cDNA; 1475 BP.  
XX AAS15360;  
XX  
XX 16-JAN-2002 (first entry)  
XX  
XX  
XX cDNA encoding human PRO1356 polypeptide.  
XX  
XX Human; PRO1356; clone DNA64886-1601; immune-related disorder;  
XX inflammatory disorder; infectious disorder; immunodeficiency disorder;  
XX autoimmune disorder; renal disease; demyelinating disease; skin disease;  
XX neoplasia; transplantation associated disease; gene therapy;  
XX immunosuppressive; anti-inflammatory; antidiabetic; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 122..814  
XX FT /\*tag= a  
XX FT /product= "PRO1356 polypeptide"  
XX FT 122..193  
XX FT /\*tag= b  
XX FT 194..811  
XX FT mat\_peptide /\*tag= c  
XX  
XX  
XX W020016740-A2.  
XX  
XX 13-SEP-2001.  
XX  
XX  
XX 01-MAR-2001; 2001WO-US006666.  
XX  
XX 03-MAR-2000; 2000US-0187202P.  
XX 21-MAR-2000; 2000US-0191015P.  
XX 30-MAY-2000; 2000WO-US014841.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 01-DEC-2000; 2000WO-US032678.  
XX  
XX  
XX (GENE) GENENTECH INC.  
XX  
XX Baton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
XX Tumias D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2001-625876/72.  
XX  
XX P-PSDB; AAU09178.

XX  
PT Nucleic acids encoding PRO polypeptides, useful for detecting and  
PT treating immune related diseases and disorders in mammals including  
PT autoimmune diseases, inflammatory diseases and asthma.  
XX  
XX Claim 2; Fig 1; 122pp; English.  
XX  
XX The present invention relates to the isolation of 9 novel human PRO  
XX polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.  
XX The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,  
XX PRO3151, PRO4322, PRO3964, PRO10008 and PRO19598. The cDNA sequences  
XX encoding these PRO polypeptides have been designated as clones DNA6486-  
XX 1601, DNA64903-1553, DNA64318-2520, DNA87997, DNA89273, DNA92223-2567,  
XX DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.  
XX vaccines) containing PRO polypeptides and methods of using these  
XX compositions are useful in the treatment and diagnosis of immune-related  
XX disorders. Such disorders include immune-mediated inflammatory disorders  
XX (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.  
XX diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),  
XX immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.  
XX rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),  
XX demyelinating diseases of the peripheral or central nervous system (e.g.  
XX Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact  
XX dermatitis), neoplasias and transplantation associated diseases. The  
XX cDNA polynucleotide sequences of the invention may be used in gene therapy.  
XX AAS15360-AAS15368 represent cDNA sequences encoding for the novel human  
XX PRO polypeptides of the invention  
XX  
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;  
XX  
XX Query Match 53.7%; Score 1472; DB 4; Length 1475;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 GCTTACGCTGAG 120  
DB 64 GCTTACGCTGAG 123  
QY 121 GGCCTCTTGGCTCCAACTTGTGGGCTACATCTAGAGCTTCTGGAGCTTTTGGGAC 180  
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QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483  
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DB 484 TGGAGTCTTTTATCTTGAAGGCTCTGGGATTCATCTGTTGCTCGAATCTTCA 543  
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QY 601 AGAGGCTCTTACTGAGGCAATTTCTCCCTGTTCTCCCTGATGAGTGAATCATCT 660
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QY 661 CTGCTTTTCTGCTCAATCCAGAGAAATGCTCCCACTACTAGATGCTCCAGGCCCA 720
DB 664 CTGCTTTTCTGCTCAATCCAGAGAAATGCTCCCACTACTAGATGCTCCAGGCCCA 723
QY 721 ACCTCTGCGACAGAGAGCTCTCCAGAGGCTGCTCACTCCCAAGTCAAGAGTGT 780
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QY 781 CAATTCCTACAGCTGACAGGGATATGTGTAAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 840
DB 784 CAATTCCTACAGCTGACAGGGATATGTGTAAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 843
QY 841 TGGGTCTGTAAATAACGTGTGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT 900
DB 844 TGGGTCTGTAAATAACGTGTGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT 903
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DB 904 GAATCGGTGACAGAGGTGCTGAGGATGAGTGACTTGTGGCATTGATGAGCAAG 963
QY 961 GCAGAAATGGGGGCTAGTGTAAACAGATGAGAGTTGAATTCAGAGAGTCTGCGCATGC 1020
DB 964 GCAGAAATGGGGGCTAGTGTAAACAGATGAGAGTTGAATTCAGAGAGTCTGCGCATGC 1023
QY 1021 GACGCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTGCTTGAATGCCCACTTCACTT 1080
DB 1024 GACGCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTGCTTGAATGCCCACTTCACTT 1083
QY 1081 GAAACCCCATCTCCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCTGTGTTTAACTGGG 1140
DB 1084 GAAACCCCATCTCCCTTAAAGCAGAGACTCAGAGATCCCTTGGCCTGTGTTTAACTGGG 1143
QY 1141 ACTGCATCCCAAAACCACTAATCAATCCCACTGACCTGCTGTGATCAAAAGCCC 1200
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DB 1324 TGGAACTTCATCCCACTCTTGTATGATCAAGTGCAGAGTCAAGTAAATTTGTGATGAA 1383
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DB 1444 CAGGAAGCAGCTGGGACATTTAAAAAATA 1475

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## RESULT 15

AAF92097 standard; cDNA; 1475 BP.

AAF92097;

15-MAY-2001 (first entry)

Human PRO1356 cDNA.

Human; PRO protein; mapping; ss.

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XX MO200116318-A2.
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XX 08-MAR-2001.
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XX 24-AUG-2000; 2000MO-US023328.
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XX 01-SEP-1999; 99MO-US020111.
XX 15-SEP-1999; 99MO-US021090.
XX 07-DEC-1999; 99US-0169495P.
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XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000MO-US004342.
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XX 21-MAR-2000; 2000US-0191007P.
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XX 22-MAY-2000; 2000MO-US014042.
XX 05-JUN-2000; 2000US-0209832P.
XX
XX (GENENTECH INC.
XX
XX Baton DL, Flvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Matanabe CK, Wood WI;
XX WPI; 2001-183260/18.
XX
XX P-PSDB; AAB87565.
XX
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping.
XX
XX Claim 2; Fig 79; 278bp; English.
XX
XX The present sequence is the coding sequence for a human PRO polypeptide
XX (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX antagonists or anti-PRO antibodies are useful for preparation of a
XX medicament useful in the treatment of a condition which is responsive to
XX the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX protein may also be employed as molecular weight markers for protein
XX electrophoresis. The PRO coding sequence has applications in molecular
XX biology, including use as hybridisation probes, and in chromosome and
XX gene mapping
XX
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
XX Query Match 53.7%; Score 1472; DB 4; Length 1475;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCACTGAGGAGAGAGTCTGAATGAGGATTAAGGTGTTCAAGAGCAAGA 60
DB 4 AGAAGTCACTGAGGAGAGAGTCTGAATGAGGATTAAGGTGTTCAAGAGCAAGA 63
QY 61 GCTTCAGCTGAAAGACAAAGGAGCACTCCCTGAAGCGTTTCTAAGAGAGTGGCCAT 120
DB 64 GCTTCAGCTGAAAGACAAAGGAGCACTCCCTGAAGCGTTTCTAAGAGAGTGGCCAT 123
QY 121 GGCCTCTCTTGGGCTCAACTGTGGGCTAATCCTAAGGCTTCTGGGCTTTTGGGCAC 180
DB 124 GGCCTCTCTTGGGCTCAACTGTGGGCTAATCCTAAGGCTTCTGGGCTTTTGGGCAC 183
QY 181 ACTGTTGCAATGCTGCTCCCACTGAGTGAATAACAACTTATATGTCGAGCATTTGT 240
DB 184 ACTGTTGCAATGCTGCTCCCACTGAGTGAATAACAACTTATATGTCGAGCATTTGT 243
QY 241 GACAGCATTTGGTTTCTCAAGGCTCTGAGTGAATGTGCCACACAGCAGGCAAT 300

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1472	53.7	1475	4 US-10-140-002-491	Sequence 491, App
2	1453.4	53.0	1524	4 US-09-663-600A-45	Sequence 45, App1
3	1393.6	50.8	1400	4 US-09-663-600A-139	Sequence 139, App
4	144.6	5.3	1253	4 US-09-673-395A-71	Sequence 71, App1
5	140.8	5.1	1705	4 US-09-205-258-106	Sequence 106, App
6	140.6	5.1	1665	4 US-09-300-958A-22	Sequence 22, App1
7	135.2	4.9	1554	4 US-09-895-652A-14	Sequence 14, App1
8	134.2	4.9	708	4 US-09-620-312D-986	Sequence 986, App
9	118.4	4.3	3443	4 US-09-886-683A-3	Sequence 3, App1
10	118.4	4.3	3483	4 US-09-130-491-3	Sequence 3, App1
11	111.2	4.1	1722	4 US-09-489-847-93	Sequence 93, App1
12	90.8	3.3	1380	4 US-09-489-847-125	Sequence 125, App
13	81.8	3.0	615	4 US-09-621-976-1835	Sequence 1835, App
14	76.8	2.8	363	2 US-08-966-316-8	Sequence 8, App1
15	75.4	2.7	441	4 US-09-404-879A-104	Sequence 104, App
16	75.4	2.7	441	4 US-09-338-933-104	Sequence 104, App
17	75.4	2.7	441	4 US-09-215-681-104	Sequence 104, App
18	75.4	2.7	441	4 US-09-216-003A-104	Sequence 104, App
19	75.4	2.7	441	4 US-09-667-857-104	Sequence 104, App
20	73.8	2.7	1165	4 US-09-603-552-2	Sequence 2, App1
21	70.8	2.6	413	3 US-09-188-930-55	Sequence 55, App1
22	70.8	2.6	413	4 US-09-332-283C-55	Sequence 55, App1
23	69	2.5	7218	1 US-08-232-463-14	Sequence 14, App1
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25	55	2.0	413	4 US-09-621-976-160	Sequence 160, App
26	48.4	1.8	7218	1 US-08-232-463-14	Sequence 14, App1
27	47.8	1.7	427	4 US-09-603-552-8	Sequence 8, App1

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C	34	37.4	1.4	5144	4	US-09-919-039-70	Sequence 70, App1
C	35	36.8	1.3	474	4	US-09-621-976-18033	Sequence 18033, A
C	36	36.8	1.3	4269	4	US-09-799-451-363	Sequence 363, App
C	37	36.6	1.3	364	4	US-09-621-976-17202	Sequence 17202, A
C	38	36.4	1.3	4897	6	5196516-7	Patent No. 5196516
C	39	35.4	1.3	44848	4	US-09-435-739-42	Sequence 42, App1
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C	41	35.2	1.3	208	4	US-09-603-552-10	Sequence 10, App1
C	42	35.2	1.3	1312	4	US-09-610-906-5	Sequence 5, App1
C	43	35.2	1.3	1312	4	US-09-976-594-346	Sequence 346, App
C	44	35.2	1.3	1354	4	US-09-610-906-2	Sequence 2, App1
C	45	34.8	1.3	25603	4	US-09-819-607-3	Sequence 3, App1

#### ALIGNMENTS

RESULT 1  
US-10-140-002-491  
Sequence 491, Application US/10140002  
Patent No. 6725730  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Denoyere, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C59  
CURRENT APPLICATION NUMBER: US/10/140,002  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 491  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-002-491  
Query Match 53.7%; Score 1472; DB 4; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
C 121 GGCTTCCTTGGCTCCCACTTGTGGCTACATCTAGGCTTGTGGGCTTTGGGAC 180  
D 124 GGCTTCCTTGGCTCCCACTTGTGGGCTACATCTAGGCTTGTGGGCTTTGGGAC 183



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DB 424 CATGATGATGACATGCTCTCTGCTCCAGGAAATCCGAGCCAAAGACAGATGGCCGATGAG 483  
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DB 1384 CTGAATTAATAACCATCTTACGATATCCAGGAAACAGAAACAGATGACAGATGGAGGA 1443  
QY 1441 CAGAAAGCAGCTTGGGACATTTTAAAAATA 1472  
DB 1444 CAGAAAGCAGCTTGGGACATTTTAAAAATA 1475

RESULT 2  
US-09-663-600A-45  
Sequence 45, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bouguetier, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 45  
LENGTH: 1524  
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NAME/KEY: sig\_peptide  
LOCATION: 160..231  
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OTHER INFORMATION: score 5.6999980926514  
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LOCATION: 1510..1515  
NAME/KEY: polyA\_site  
LOCATION: 1506..1519  
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US-09-663-600A-45

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DB GTACAGAGCTTGGCTTCTCAAGGAGCTGAGATGAGTGCACACAGAGAGAGC 399  
QY 340 ATCAACCAAGTGAATCTATAGCACTTCTGGGCTTGGCTGATCCAGAGTGC 418  
DB ATCAACCAAGTGAATCTATAGCACTTCTGGGCTTGGCTGATCCAGAGTGC 459  
QY 359 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478  
DB CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519  
QY 419 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 538  
DB GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579  
QY 479 GGTGAGTCTTTTCACTTCTTGAAGGCTCTGGGATTCATTCCTGTTGGCTGAATCT 598  
DB GGTGAGTCTTTTCACTTCTTGAAGGCTCTGGGATTCATTCCTGTTGGCTGAATCT 639  
QY 539 CATGGATCTTACGAGGATCTTACTACCACTGGTGTCTGACAGATGAATTTGAGATT 658  
DB CATGGATCTTACGAGGATCTTACTACCACTGGTGTCTGACAGATGAATTTGAGATT 699  
QY 599 GAGAGGCTTTTACTTGGGATTAATTTCTTCTGTTCTTCTGATGATGATGATGAT 718  
DB GAGAGGCTTTTACTTGGGATTAATTTCTTCTGTTCTTCTGATGATGATGATGAT 759  
QY 640 GAGAGGCTTTTACTTGGGATTAATTTCTTCTGTTCTTCTGATGATGATGATGAT 778  
DB GAGAGGCTTTTACTTGGGATTAATTTCTTCTGTTCTTCTGATGATGATGATGAT 819  
QY 659 CTCTGCTTTCTGCTCATCCAGAGAAATGCTCAACTACTAGATGCTCAAGGCC 759  
DB CTCTGCTTTCTGCTCATCCAGAGAAATGCTCAACTACTAGATGCTCAAGGCC 799

DB 700 CTCTGCTTTCTGCTCATCCAGAGAAATGCTCAACTACTAGATGCTCAAGGCC 759  
QY 719 CAACCTCTTGGCAAGAGAGCTCTCAAGGCTGTCAACTCTCCAAAGTCAAGATGAG 778  
DB CAACCTCTTGGCAAGAGAGCTCTCAAGGCTGTCAACTCTCCAAAGTCAAGATGAG 819  
QY 779 TTCAATTCCTACAGCTGACAGGATATGTGTAAGAACAGAGGAGGAGAGCTGGGAGT 838  
DB TTCAATTCCTACAGCTGACAGGATATGTGTAAGAACAGAGGAGGAGAGCTGGGAGT 879  
QY 839 GCTGGTCTGTGTAAGAACAGTGAACAGCCTCGAGGAGGAGAGGAGAGCTGAACA 898  
DB GCTGGTCTGTGTAAGAACAGTGAACAGCCTCGAGGAGGAGAGGAGAGCTGAACA 939  
QY 899 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958  
DB CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999  
QY 959 AGCAGAGAAATGGGAGGAGTGTAAAGAGATGAGAGTGAATGACCAAGATGCTGCCAT 1018  
DB AGCAGAGAAATGGGAGGAGTGTAAAGAGATGAGAGTGAATGACCAAGATGCTGCCAT 1059  
QY 1019 GCCAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAAGCTTCAAC 1078  
DB GCCAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAAGCTTCAAC 1119  
QY 1079 TTGAATCCCATTCCTTAAGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAG 1138  
DB TTGAATCCCATTCCTTAAGAGAGATGAGAGATGAGATGAGATGAGATGAGATGAG 1179  
QY 1139 GGAATCCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1198  
DB GGAATCCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1239  
QY 1180 GATCTCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258  
DB GATCTCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1299  
QY 1199 CTTCTCTGCTGAGTGTGCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1318  
DB CTTCTCTGCTGAGTGTGCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1359  
QY 1259 GCTTTTGTGGAGATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1378  
DB GCTTTTGTGGAGATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1419  
QY 1319 CTTGAATCCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438  
DB CTTGAATCCATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1479  
QY 1420 AACTGAATTAACATCTTAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1483  
DB AACTGAATTAACATCTTAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1524  
QY 1439 GACAG 1483  
DB GACAG 1524

RESULT 3  
US-09-663-600A-139  
Sequence 139, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclelet, Aymeric  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.053.CIP  
CURRENT FILING DATE: 2000-09-15  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 139  
LENGTH: 1400  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 36..107  
OTHER INFORMATION: Von Heljne matrix  
OTHER INFORMATION: score 5.6999980926514  
OTHER INFORMATION: seq ILGLGLTLVA/ML  
NAME/KEY: polyA\_signal  
LOCATION: 1302..1307  
NAME/KEY: polyA\_site  
LOCATION: 1389..1400  
US-09-663-600A-139

Query Match 50.8%; Score 1393.6; DB 4; Length 1400;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1396; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

84 CAGTCCCTGAAGACGCTTCTTCTGAGAGGTCGTCATGCGCTCTCTTGGGCTTCAACTTG 143  
1 CAGTCCCTGAAGACGCTTCTTCTGAGAGGTCGTCATGCGCTCTCTTGGGCTTCAACTTG 60  
144 TGGGCTCAATCCATGAGGCTTCTGAGGCTTCTTGGGCACTGCTGTCATGCTGCTCCCA 203  
61 TGGGCTCAATCCATGAGGCTTCTGAGGCTTCTTGGGCACTGCTGTCATGCTGCTCCCA 120  
204 GCTGGAAGAAAGAGTCTTATGTCGTCGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 263  
121 GCTGGAAGAAAGAGTCTTATGTCGTCGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 180  
264 GCTCTGAGATGAGATGTCGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 323  
181 GCTCTGAGATGAGATGTCGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 240  
324 CCGTTCGAGGCTGCGGCTGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 383  
241 CCGTTCGAGGCTGCGGCTGTCAGCATTTGTCAGGAGTTCCTTCCAAAG 300  
384 CATCTCTCTCTGAGGCTGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 443  
301 CATCTCTCTCTGAGGCTGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 360  
444 AGGATTCGAGGCTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 503  
361 AGGATTCGAGGCTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 420  
504 GCGTTCGAGGCTGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 563  
421 GCGTTCGAGGCTGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 480  
564 CACCACTGAGGCTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 623  
481 CACCACTGAGGCTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 540  
624 TTTCTTCCTGTCGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 683  
541 TTTCTTCCTGTCGTCATTTCTGTCGTCAGGAGTTCCTTCCAAAG 600  
684 GAAATGCTCAACTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 743  
601 GAAATGCTCAACTGTCAGGAGTTCGTCAGGAGTTCCTTCCAAAG 660

744 CAAGGCTGTCACCTTCCAAAGTCAGAGTGTTCATTTCTTACGCTTACAGGGT 803  
661 CAAGGCTGTCACCTTCCAAAGTCAGAGTGTTCATTTCTTACGCTTACAGGGT 720  
804 ATGTGTGAAGAACCAAGGGGTCAGAGTGTGGGGTGTGGGGTGTGGAAACAGGAGC 863  
721 ATGTGTGAAGAACCAAGGGGTCAGAGTGTGGGGTGTGGGGTGTGGAAACAGGAGC 780  
864 AGCAGCCGAGGGGTCAGAGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 923  
781 AGCAGCCGAGGGGTCAGAGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 840  
924 GAGATGAGCTGCTTGGGCTGTCATTTGTCAGGAGTTCGTCAGGAGTTCGTCAGG 983  
841 GAGATGAGCTGCTTGGGCTGTCATTTGTCAGGAGTTCGTCAGGAGTTCGTCAGG 900  
984 AGCATCAGGTTGAATTTGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1043  
901 AGCATCAGGTTGAATTTGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 960  
1044 TGTGCTCCCTGCTGCTTAAAGTCCCAAGCTTCACTTGAACCCCACTTCAAGCCAG 1103  
961 TGTGCTCCCTGCTGCTTAAAGTCCCAAGCTTCACTTGAACCCCACTTCAAGCCAG 1020  
1104 GACTCAGAGATTCCTTGGGCTTCTGTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1163  
1021 GACTCAGAGATTCCTTGGGCTTCTGTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1080  
1164 CACATCCCACTGACCTGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1223  
1081 CACATCCCACTGACCTGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1140  
1224 TAGCTCATTTGTCGAGGATGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1283  
1141 TAGCTCATTTGTCGAGGATGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1200  
1284 ACTTCTCAAGCTTCCCTTCAAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1343  
1201 ACTTCTCAAGCTTCCCTTCAAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1260  
1344 TATGACTTCAAGCTTCCCTTCAAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1403  
1261 TATGACTTCAAGCTTCCCTTCAAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1320  
1404 ATCCAGGAGAACAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1463  
1321 ATCCAGGAGAACAGAGATTCGTCAGGAGTTCGTCAGGAGTTCGTCAGGAGTTCGTCAGG 1380  
1464 AAAAAATTAATAATGAAAA 1483  
1381 AAAAAATTAATAATGAAAA 1400

RESULT 4  
US-09-673-395A-71  
Sequence 71, Application US/09673395A  
Patent No. 6620923  
GENERAL INFORMATION:  
APPLICANT: SPECHT, THOMAS  
APPLICANT: HINZMANN, BERND  
APPLICANT: SCHMITT, ARMIN  
APPLICANT: PILARSKY, CHRISTIAN  
APPLICANT: DAHL, EDGAR  
APPLICANT: ROSENTHAL, ANDRE  
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE  
FILE REFERENCE: ALBRE-12  
CURRENT APPLICATION NUMBER: US/09/673,395A  
CURRENT FILING DATE: 2000-10-17  
NUMBER OF SEQ ID NOS: 637  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 71  
LENGTH: 1253

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-71

Query Match
Best Local Similarity 5.3%; Score 144.6; DB 4; Length 1253;
Matches 310; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 109 GAGGTGCGCATGAGCTCTCTGTTGCTCCCACTGTTGGGCTTAACCTTGAAGCTTGGG 168
DB 336 GAGGGCGAATATGCGCAATTCGGGCTGCAAGTCTGAGGCTTCTCCATGAGCCCTGGG 395
QY 169 GCTTTTGGGCACTGTTGCCATGCTGCTCCCAAGCTGAAAACAAGTTCTTATGTCG 228
DB 396 CTGGGGTGGTCTGTGGCTGCTGACCGCGCATCCGCAATGGCAATGAGTCTCTATGGGG 455
QY 229 TGCAGCATTTGTACAGCAAGTGTGCTTCTCCAAAGGCTCTGATGTAATGTGCACACA 288
DB 456 TGAACATCATCATACGGCCCAAGGCAATGTAACAAGGGCTGTGATGACTGCGTCAAGCA 515
QY 289 CAGCAGGCGATCACCAGTGTGATCTATAGACACCTTCTGGGCTGCGCGGTGACAT 348
DB 516 GAGCAGGGGATATGAGCTGCAAAATGTAAGACTGCTGCTGCTGCTGCTGCTGCTGCT 575
QY 349 CCAGGCTGCCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
DB 576 GCGAGGCGCATGAGCCCTTAATGGTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 635
QY 409 CTCTGTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465
DB 636 GGCACAGATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
QY 466 AGTGGGGTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
DB 696 TATAGCATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
QY 526 TGCTTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
DB 756 CTCTGGTATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
QY 586 GAAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
DB 816 TAAATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
QY 646 AGCTGATCATCTCTGCTTTCTG 672
DB 876 GAGAGTGAAGTCTCTCTGTTCTG 902

RESULT 5
US-09-205-258-106
; Sequence 106, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: SITE  
LOCATION: (724)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-205-258-106

Query Match 5.1%; Score 140.8; DB 4; Length 1705;  
Best Local Similarity 50.7%; Pred. No. 1,9e-33;  
Matches 334; Conservative 1; Mismatches 324; Indels 0; Gaps 0;

82 AGCAGTCCCTGAAGACGCTTCTACTAGAGAGTCTGCATGAGCCCTCTCTGAGCCCTCAACT 141  
172 AGCCTTCAAGTCTCTCACTCCGCGAGACGCTGAACATGAGCTTCTCAAGGCTACAGGT 231  
142 TGTGGCTACATCTAGACCTTCTGAGGCTTTTGGGCACTGCTTCCATGCTGCC 201  
232 AATGGGATGCGCGTGGCCGCTCTGAGGCTGAGGCTGCTGATGCTGAGCTGCGGCTGCC 291  
202 CAGCTGAAAAACAAGTTCTTATGCTGCTGCAAGCATTTGACAGAGTTGGCTTCCAA 261  
292 CATGTGGCGCGTACGCGCTTCACTCGGCAACATTTGTCACTCGAGACATCTGGGA 351  
262 GGGCTCTGATGGAATGTCACACACAGACAGGATGACCCAGTGTGACATCTATAG 321  
352 GGGCTATGATGATGCTGCTGCTGAGAGACGAGCAAGTGCAGAGTGAAGGTGACGA 411  
322 CACCTTCTGGGCTGCGCTGATCATCAGGCTGCGGCAAGCATGATGATCATCAG 381  
412 CTGGCTGCTGCACTGCGAGAGACCTGAGGGGCGCGCTGCTCATCATCAGCAT 471  
382 TGCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441  
472 CATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531  
442 CAGGAATCCCGAGCCAAAGACAGATGAGGAGTGAAGTGTCTTTTCACTCTTG 501  
532 GAGGATGAAGAGCGCCAGAGCAAGCATGATGAGGAGGCTGCTGCTGCTGCTGCTG 591  
502 AGGCTCTGAGGATTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561  
592 CGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651  
562 CTCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
652 CATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711  
622 TATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681  
712 GGGCGCTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771  
682 GAGAAATCGCTCAACTACTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740  
772 CACAGACAAAGCTTACTCGCGCAAGTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830

RESULT 6  
US-09-300-958A-22  
Sequence 22, Application US/09300958A  
Patent No. 6495319

GENERAL INFORMATION:  
APPLICANT: McCrelland, Michael  
APPLICANT: Weissh, John  
APPLICANT: Tremlie, Thomas  
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
FILE REFERENCE: P-PH 3457  
CURRENT APPLICATION NUMBER: US/09/300,958A  
CURRENT FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/083,331  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/098,070  
PRIOR FILING DATE: 1998-08-27  
PRIOR APPLICATION NUMBER: 60/118,624  
PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 85  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 22  
LENGTH: 1665  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-300-958A-22

Query Match 5.1%; Score 140.6; DB 4; Length 1665;  
Best Local Similarity 50.8%; Pred. No. 2.1e-33;  
Matches 335; Conservative 0; Mismatches 324; Indels 0; Gaps 0;

82 AGCAGTCCCTGAAGACGCTTCTACTAGAGAGTCTGCATGAGCCCTCTCTGAGCCCTCAACT 141  
146 AGCCTTCAAGTCTCTCACTCCGCGAGACGCTGAACATGAGCTTCTCAAGGCTACAGGT 205  
142 TGTGGCTACATCTAGACCTTCTGAGGCTTTTGGGCACTGCTTCCATGCTGCC 201  
206 AATGGGATGCGCGTGGCCGCTCTGAGGCTGAGGCTGCTGATGCTGCTGCGGCTGCC 265  
202 CAGCTGAAAAACAAGTTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261  
266 CATGTGGCGCGTACGCGCTTCACTCGGCAAGCATTTGACAGAGTTGAGCTTGGGA 325  
262 GGGCTCTGAGTGAATGTCACACACAGACAGGATGACCCAGTGTGACATCTATAG 321  
326 GGGCTATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385  
322 CACCTTCTGGGCTGCGCTGATCATCAGGCTGCGGCAAGCATGATGATCATCAG 381  
386 CTGGCTGCTGCACTGCGAGAGACCTGAGGGGCGCGCTGCTCATCATCAGCAT 445  
382 TGCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441  
446 CATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 505  
442 CAGGAATCCCGAGCCAAAGACAGATGAGGAGTGAAGTGTCTTTTCACTCTTG 501  
506 GAGGATGAAGAGCGCCAGAGCAAGCATGATGAGGAGGCTGCTGCTGCTGCTGCTG 565  
502 AGGCTCTGAGGATTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561  
566 CGGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625  
562 CTCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
626 CATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685  
622 TATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681  
686 GGGCGCTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745  
682 GAGAAATCGCTCAACTACTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740  
746 CACAGACAAAGCTTACTCGCGCAAGTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804

RESULT 7  
US-09-895-652A-14  
Sequence 14, Application US/09895652A  
Patent No. 6774223

GENERAL INFORMATION:  
APPLICANT: Macina, Roberta  
APPLICANT: Pillai, Rageswari  
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
FILE REFERENCE: DEX-0211  
CURRENT APPLICATION NUMBER: US/09/895,652A  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: 60/214,515  
PRIOR FILING DATE: 2000-06-28  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 14  
LENGTH: 1554  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1544)  
US-09-895-652A-14

Query Match  
Best Local Similarity 54.8%; Pred. No. 1e-31;  
Matches 311; Conservative 0; Mismatches 253; Indels 4; Gaps 2;

4.9%; Score 135.2; DB 4; Length 1554;  
Query 109 GAGGTGCGCATGGGCTCTGCTGGCCCTCCAGCTGTGGGGCTTACATCTTGAAG-CTTTTGG 167  
Db 424 GAGGGCGGAATGGCCATTGCGGCTCGAGCTTCTGAGCTTCTCCATGGGCTCTGCG 483  
Qy 168 GGGCTTTGGGCACTGGTTCATGCTGCTGCCAGCTGGGAAAACAAGTTCTTATGTCG 227  
Db 484 GCTGGGTGGGTCTGGTGGCCCGACCGCCATCCCGGAGATGAGCTCTATGCGG 543  
Qy 228 GTGGCAGCATTTGACAGCAGTTGGCTTCTCCAGGGCTCTGGATGGATGGCCACAC 287  
Db 544 GTGACACATCATCACGCGCCAGGCGCATGACAGGGGCTGTGGATGAGCTGGCTACGC 603  
Qy 288 ACAGCAGGCGATCACCAGTGTGACATCTATAGCACCCCTTGGGGCTGGCCGCTGACA 347  
Db 604 AGAGCAGGGAGATGATAGCTGCAAAATGACAGCTGGTCTGCTGCTGCTGCTGCTG 663  
Qy 348 TCCAGCTGCGCCAGGCGCATGATGATGACATCTCCCTGGGCTGACATTA 407  
Db 664 TGACAGGCGCATCGAGCCCTATAGTGTGCTCCCGTGGTGGCTTCTGGCCATGTTTG 723  
Qy 408 TCTGTGTGGGGCATGATGACAGCTCTTTCGCAAGATCCGAG--CCAAAGACA 464  
Db 724 TGCGCAGATGGGCGATGATGACAGCGCTGTGGGGGAGACAAAGTGAAGAGGCC 783  
Qy 465 GAGTGGGGGTAGCAGGTGGAGTCTTTTTCATCCCTTGGAGGCTCTGGATCTTCTG 524  
Db 784 GTATAGCATGGGTGAGGCGATATTTTTCATCGGGCTTGGCCGCTTGGTACTT 843  
Qy 525 TTGGCTGGAATCTTATGAGATCTTACGAGCTTCTACTCAGCACTGGTGGCTGACACA 584  
Db 844 GCTCTGTGTATGGCATCAATTTGTCAAGACTTTTAACTTTATCCCTTACCAACA 903  
Qy 585 TGAATTTGAGATGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGA 644  
Db 904 TTAAATATGAGTTTGGCCCTGCGCATTTATTTGGCTGGGCGAGGCTGAGCTATGATCC 963  
Qy 645 TAGCTGGAATCATCTCTGCTTTTCTG 672  
Db 964 TGGAGGTGACATGCTCTCTCTGTTCTG 991

## RESULT 8

US-09-620-312D-986  
Sequence 986; Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Abundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yunding  
APPLICANT: Wang, Duntui

APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghaast  
APPLICANT: Demanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP28  
CURRENT APPLICATION NUMBER: US/09/620,312D  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pc FL\_genes Version 1.0  
SEQ ID NO 986  
LENGTH: 708  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (46)..  
US-09-620-312D-986

Query Match  
Best Local Similarity 50.7%; Pred. No. 1.2e-31;  
Matches 322; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

4.9%; Score 134.2; DB 4; Length 708;  
Query 116 GCCATGGCTCTCTTGGCTCCCACTTGGGGCTATAGCCCTTGGGGCTTTTG 175  
Db 43 GCCATGGCTCTCTCGAATGAGATCTGGAGTGTCTGACATGCTGGGCTGGTG 102  
Qy 176 GGCACTGGTTCATCATGCTGCTCCCGAGCTGAGAAAACAAGTTCTTATGCTGGCAGC 235  
Db 103 AATGGCTGTCTCTGTGCTGCTCCCATGTGAGAGTACCGCTTTCATCGCAAGC 162  
Qy 236 ATTGTGACAGAGTGGCTTCTCCAGGGCTCTGATGATGATGACACACAGACA 235  
Db 163 ATGTGTGGCCAGAGTGTGAGAGGGCTGTGATGTCGTGTGTGACAGAGCACC 222  
Qy 296 GGCATCACCAAGTGTGATCATCTATAGCACCTTCTGGGCTGCGCCCTGACATCCAGGCT 355  
Db 223 GGCAGATGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 282  
Qy 356 GCCAGGCGCATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 415  
Db 283 GCAAGTGGCTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 342  
Qy 416 GTGGGCGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 475  
Db 343 GCTGGGCGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 402  
Qy 476 GCAAGTGAAGTCTTTTATCATCTTGAAGGCTCTCTGGAGTCAATCTCTGTGCTGAAT 535  
Db 403 ACCCTGGAGTGTCTTGTGATCTGAGGGTCTGACGCTATCCCGTGTGTGACG 462  
Qy 536 CTTCATGGAATCTGAGGAGCTTCTACTACAGCTGGTGGCTGACAGCATGAATTTAG 595  
Db 463 GCGATGCGGTGATCGGAGCTTCTATACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGT 522  
Qy 596 ATTGAGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGAATC 655  
Db 523 CTGGGGGCTCTCTCTACTTGGGCTGGGGGCGCTCAAGGCTTTTGTGTGTGTGTGTGTGT 582  
Qy 656 ATCTCTGCTTTTCTGTCTATCTCCAGAGAAATGCTCTCAACTATGATGCTTACCA 715  
Db 583 TTGCTGTGTGACATGCTGCGGCTGCGGGGGTCCAGGGCCCAAGCATTAATGCGCGC 642  
Qy 716 GCCCACTCTGCGCAAGAGAGTCTCCAAAGGC 750  
Db 643 TACTCAACATCTGCGCTGCGCATCTCTCGGGGGC 677

## RESULT 9

```
US-09-886-683A-3
; Sequence 3, Application US/0988683A
; Patent No. 6627439
; GENERAL INFORMATION:
; APPLICANT: Hoevel, Thorsten
; APPLICANT: Koch, Stefan
; APPLICANT: Kubbies, Manfred
; APPLICANT: Mundigl, Olaf
; APPLICANT: Rueger, Petra
; TITLE OF INVENTION: Antibodies against SEMPL (p23)
; FILE REFERENCE: Case 20692
; CURRENT APPLICATION NUMBER: US/09/886,683A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: EP00113344.6
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: EP01107799.7
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(853)
; US-09-886-683A-3
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Query Match 4.3%; Score 118.4; DB 4; Length 3443;
Best Local Similarity 52.0%; Pred. No. 3,6e-26;
Matches 291; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
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QY 116 GCCATGGCTCTCTTGGCTTCCAGCTTGTGGCTACATCTAGGCTTCTGGGCTTTTG 175
DB 218 GTATGGCCCAACGGGGGCTGACGCTTGGGCTTACTTCGCTTCTGGATGATC 277
QY 176 GGCACTGTTGGCTGCTGCTCCCACTGGAACAACTTATGTCGCTGCTGCTGCT 235
DB 278 GGGGCTCTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 337
QY 236 ATTGTGACAGAGTGGCTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 295
DB 338 ATGTGATCCGCGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
QY 296 GGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
DB 398 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 457
QY 356 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
DB 458 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 517
QY 416 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
DB 518 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 577
QY 473 GTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
DB 578 GTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 637
QY 533 AATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
DB 638 TATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 697
QY 593 GAGATTTGAGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
DB 698 GAGATTTGAGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 757
QY 653 ATCATCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
DB 758 GCCCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
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RESULT 10
US-09-130-491-3
; Sequence 3, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodheart, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (240)..(872)
; US-09-130-491-3
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Query Match 4.3%; Score 118.4; DB 4; Length 3483;
Best Local Similarity 52.0%; Pred. No. 3,7e-26;
Matches 291; Conservative 0; Mismatches 266; Indels 3; Gaps 1;
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QY 116 GCCATGGCTCTCTTGGCTTCCAGCTTGTGGCTACATCTAGGCTTCTGGGCTTTTG 175
DB 237 GTATGGCCCAACGGGGGCTGACGCTTGGGCTTACTTCGCTTCTGGATGATC 296
QY 176 GGCACTGTTGGCTGCTGCTCCCACTGGAACAACTTATGTCGCTGCTGCTGCTGCT 235
DB 297 GGGGCTCTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 356
QY 236 ATTGTGACAGAGTGGCTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 295
DB 357 ATGTGATCCGCGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
QY 296 GGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
DB 417 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 476
QY 356 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
DB 477 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536
QY 416 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
DB 537 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596
QY 473 GTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532
DB 597 GTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 656
QY 533 AATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
DB 657 TATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
QY 593 GAGATTTGAGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
DB 717 GAGATTTGAGAGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
QY 653 ATCATCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
DB 777 GCCCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
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RESULT 11
US-09-489-847-93
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/ Sequence 93, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 93
/ LENGTH: 1722
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-93
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Query Match 4.1%; Score 111.2; DB 4; Length 1722;
Best Local Similarity 50.0%; Pred. No. 4.1e-24;
Matches 275; Conservative 1; Mismatches 274; Indels 0; Gaps 0;

QY 116 GCCATGCGCTCTCTGCGCTCCCACTGTGGGCTGACATCTTAGCCCTTCTGGGCTTTG 175
DB 458 GCCATGCGGCTCCGACGGTGGAGATCTTGGCTGTGCTGTGGGCTGGGCTGGGG 517
QY 176 GGCACTGTTGCTCCATGCTGCTCCCGAGCTGAAACAAATTCTATGTCGGTCCAGC 235
DB 518 GGTCTGATCTGTGGCGTGGGGCTGCCATGTGGAGGTGACCGCTTCTTGACCAAC 577
QY 236 ATTGTGACAGCAGTTGGCTTCTCCAGGGCTCTGTGATGTGATGTGCACACACAGACA 295
DB 578 ATGTGACGCGCAGACCACTGTGAAAGGGCTGTGATGTGTCGTGTGACAGACAC 637
QY 296 GGCATCCACCAAGTGTGACATCTATAGCACTTGTGGGCTGCGCGGTGACATCCAGGT 355
DB 638 GGGCACATGTGACAAAGTGTAGCACTGGTGTGCTGTGACACCGAGGTGACAGCG 697
QY 356 GCCCAGGCGCATGATGTGACATCCAGTGAATCTCTCCCTGCGCTGCATTATCTGTG 415
DB 698 GCGCGGGCGCTCACCGTAGGCGCGTGTGCTGGCGTTCTTGCGCTTCTGTACCTTG 757
QY 416 GTGGGCAATGATGACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTA 475
DB 758 GCGGGCGCGAGTGCACCACTGCTGTGCGCCCGGCGCCGAGCGCGTGTGGCCCTC 817
QY 476 GCAAGTGAATCTTTTCACTTGTGAGGCGCTCTGGGATTCATCTCTGTGCTGGAAT 535
DB 818 ACCGGAAGCGTGTCTACCTGTTTGTGGGCTGTGCGCTGTGCGCACTCTGTGTTTC 877
QY 536 CTTCATGGATCTTACAGGGAATTCTACTACCACTGTGAGCTGTGACAGATGAATTGAG 595
DB 878 GCCAATTTGTCGCGAGTTTACGACCCGCTGTGCGCGGTGTGCGAGAAATTACGAG 937
QY 596 ATTGAGAGGCTCTTTAATTGGGCAATATTTCTTCCGTGTTCTCCGTATAGCTGGAATC 655
DB 938 CTGGGGCGACGGCTGTACATGCGTGGGCGGCGACCGCGGCTGTCAATGTAGGGGCTGC 997
QY 656 ATCTCTGCT 665
DB 998 CTCTGTGCT 1007
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RESULT 12
US-09-489-847-125
/ Sequence 125, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 125
/ LENGTH: 1380
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-489-847-125
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Query Match 3.3%; Score 90.8; DB 4; Length 1380;
Best Local Similarity 50.2%; Pred. No. 9.6e-18;
Matches 276; Conservative 0; Mismatches 272; Indels 2; Gaps 2;

QY 116 GCCATGCGCTCTCTGCGCTCCCACTGTGGGCTGACATCTTAGCCCTTCTGGGCTTTG 175
DB 132 GCCATGCGGCTCCGACGGTGGAGATCTTGGCTGTGCTGTGGGCTGGGCTGGGG 191
QY 176 GGCACTGTTGCTCCATGCTGCTCCCGAGCTGAAACAAATTCTATGTCGGTCCAGC 235
DB 192 GGTCTGATCTGTGGCGTGGGGCTGCCATGTGGAGGTGACCGCTTCTTGACCAAC 251
QY 236 ATTGTGACAGCAGTTGGCTTCTCCAGGGCTCTGTGATGTGATGTGCACACACAGACA 295
DB 252 ATGTGACGCGCAGACCACTGTGAAAGGGCTGTGATGTGTCGTGTGACAGACAC 311
QY 296 GGCATCCACCAAGTGTGACATCTATAGCACTTGTGGGCTGCGCGGTGACATCCAGGT 355
DB 312 GGCA-CATGCAATGTGACAAAGTGTAGCACTGGTGTGCTGTGACACCGAGGTGACAGCG 370
QY 356 GCCCAGGCGCATGATGTGACATCCAGTGAATCTCTCCCTGCGCTGCATTATCTGTG 415
DB 371 GCGCGGGCGCTCACCGTAGGCGCGTGTGCTGGCGTTCTTGCGCTTCTGTACCTTG 430
QY 416 GTGGGCAATGATGACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGTA 475
DB 431 GCGGGCGCGAGTGCACCACTGCTGTGCGCCCGGCGCCGAGCGCGTGTGGCCCTC 490
QY 476 GCAAGTGAATCTTTTCACTTGTGAGGCGCTCTGGGATTCATCTCTGTGCTGGAAT 535
DB 491 ACCGGAAGCGTGTCTACCTGTTTGTGGGCTGTGCGCTGTGCGCACTCTGTGTTTC 550
QY 536 CTTCATGGATCTTACAGGGAATTCTACTACCACTGTGAGCTGTGACAGATGAATTGAG 595
DB 551 GCCAATTTGTCGCGAGTTTACGACCCGCTGTGCGCGGTGTGCGAGAAAGTACGAG 610
QY 596 ATTGAGAGGCTCTTTAATTGGGCAATATTTCTTCCGTGTTCTCCGTATAGCTGGAATC 655
DB 611 CTGGGGCGA-CGCTGTACATGCGCTGGGCGGCGACCGCGGCTGTCAATGTAGGGGCTGC 669
QY 656 ATCTCTGCT 665
DB 670 CTCTGTGCT 679
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RESULT 13  
US-09-621-976-1835  
; Sequence 1835, Application US/09621976  
; Patent No. 663063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET 054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; NUMBER OF SEQ ID NOS: 2000-07-21  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1835  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 173..511  
; NAME/KEY: sig\_peptide  
; LOCATION: 173..409  
; OTHER INFORMATION: Von Heljne matrix  
; OTHER INFORMATION: score 4.30000019073486  
; OTHER INFORMATION: seq YDSILALSPDLQA/AR  
US-09-621-976-1835

Query Match 3.0%; Score 81.8; DB 4; Length 615;  
Best Local Similarity 51.6%; Pred. No. 3.7e-15;  
Matches 209; Conservative 1; Mismatches 193; Indels 2; Gaps 1;

QY 119 ATGGCCCTCTTGGCCCTCCAACTGTGGGCTACATCTTGGAGCTTTGGCC 178  
DB 173 ATGGCAACCCATGCTTGAATGCTGGGCTTTTGGTGTGGAAATGGTGGC 232  
QY 179 ACACTGGTTCCTGCTGCTCCCACTGAGAAACAAGTTCTTATGTGGTCCAGATT 238  
DB 233 ACATGGCTGTCACTGTGATGCTCAGTGAAGATGTGGCTTCATTGAAACAATC 232  
QY 233 GTGACAGATTGGCTTCTCCAGGGCTCTGATGAAATGTGCCACACACAGACAGC 298  
DB 293 GTGGTTTTTAAACCTTCTGGGAAGACTGTGATGAATGCTGAGGACAGCTAAC 352  
QY 299 ATACCCAGTGTGACATCTATAGCACTTCTGGGCTGCGCGGTGACATCCAGGCTGCC 358  
DB 353 AGAATGACGTGCAAAATCTATGATTCCTCTGCTCTTTCTCGGACCTACAGGACGCC 412  
QY 359 CAGGCCATGATGTGATCATCACTGATCTCTCTGCTGCTGATTAATCTGTGTG 418  
DB 413 AGAGACATGATGTGTGTGCTGCTCGTATGCTCTTGTGCTTATGATGGCATCTT 472  
QY 419 GGCATGATGACACAGCTTCTGCGAGGAATCCGA--GCCAAGACAGAGTGGCGTAG 476  
DB 473 GGCATGAATASACAGGTGACGCGGGGACATGAAAGGAGGCTCACATCTGCTGA 532  
QY 477 CAGGTGAGTCTTTTCTATCTTGGAGGCTCTCTGGGATTCATTC 521  
DB 533 CGGCTGGAATCATCTTATCATCGCGGACATGATGTGTCTATCC 577

RESULT 14  
US-08-966-316-8  
; Sequence 8, Application US/08966316  
; Patent No. 5932445  
; GENERAL INFORMATION:  
; APPLICANT: Lai, Preeti  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Reddy, Roopa  
; APPLICANT: Murty, Lynn B.  
; APPLICANT: Mathur, Preete

TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/966,316  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0424 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: HMT3AZT01  
CLONE: 2417676  
US-08-966-316-8

Query Match 2.8%; Score 76.8; DB 2; Length 363;  
Best Local Similarity 55.7%; Pred. No. 9.5e-14;  
Matches 147; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 116 GCCATGCGCTCTCTTGGCTCCAACTGTGGGCTACATCTTGGGCTTTGG 175  
DB 45 GCATGCGCTCTGCGGAAATGACATCTGAGAGTGTCTGTGACACTGCTGGGCTGG 104  
QY 176 GGCACACTGTGTCATGCTGCTCCCACTGGAATAACAAGTTCTTATGTGTGCGCAGC 235  
DB 105 AATGCGCTGTCTCTGTCGCTGCTGCTGATGTGAAGTGAACGCTTTCATTCGGAACGC 164  
QY 236 ATTGTGACAGCAATGATGCTTCTCCAGGGCTCTGATGAAATGTGCCACACACAGACA 295  
DB 165 ATGTGTGTGCGCCAGATGTGTGTGGAGGCTGTGTGATGTCTGTGTGTGACAGACACC 224  
QY 296 GGCATCAACCAATGTGACATCTATAGCACTTCTTGGGCTGCGCTGATCAATCCAGGCT 355  
DB 225 GGCATATGACAGTGAAGGTGATGACATGCTGCGCTGCAAGACCTGACAGAGCTG 284  
QY 356 GCCCAGGCAATATGTGACATCC 379  
DB 285 GCACGTGCGCTCTGTGTATTCGCC 308

RESULT 15  
US-09-404-879A-104  
; Sequence 104, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.

```

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITL OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.46252
: CURRENT APPLICATION NUMBER: US/09/404,879A
: CURRENT FILING DATE: 1999-09-24
: NUMBER OF SEQ ID NOS: 393
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 104
: LENGTH: 441
: TYPE: DNA
: ORGANISM: Homo sapien
: IS-09-404-879A-104

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Query Match	2.7%	Score	75.4	DB	4	Length	441
Best Local Similarity	53.6%	Pred. NO.	3e-13				
Matches 157, Conservative						Indels	0
						Gaps	0

QY	82	AGCAGTCCCTGAAGACGCTTTACTAGAGAGCTGTGCACATGAGCCTCTCTTGAGCCTCCAACT	141
Db	146	AGCCTTCACAGGTCTTCACTCCCGGTGACGCTGAACAAATGACCTCCATGAGGCTTACAGGT	205
QY	142	TGTGGGCTACATCTTAGGCGCTTCTGAGGAGCTTTTGGGACACATGGTTCACATGCTGCTCC	201
Db	206	AATGGGCAATCGGCGTGGCGCTCTGTGGGCTGTGGCGCTCATCTGTGCTGCGCGCTGCC	265
QY	202	CAGCTGSAAMAAAGTTCTTATGTGCGGTGCCAGCATTTGTGAACAGCAGTTGGCTTCCAA	261
Db	266	CATGTGGGGCGGTGACGGCCTTATGTGGGACAGCAATTGTGACCTTGCAGACCATTTGGGA	325
QY	262	GGGCGCTGTGATGGAATGTGCACACACAGCAACAGGCATCACCCAGTGTGACATCTTAATAG	321
Db	326	GGGCGCTTATGATGAATCTGGTGTGGTAGAGACACCGGCGACAGATCAGTGGACAGGTGTACGA	385
QY	322	CACCTTTCTGGGCGCTGCCGCTGACATCCAGGCTGCCCAAGCCATATATGTGA	374
Db	386	CTGGCTGTGTGGGACATGGCCGACAGACCTTGAAGGGGGCGCGCCTTGTCATCA	438

Search completed: October 30, 2004, 09:12:19  
Job time : 295 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 13:46:35 ; Search time 12494 Seconds  
(without alignments)  
7997.258 Million cell updates/sec

Title: US-09-787-677A-7  
Perfect score: 2742  
Sequence: 1 agagagcagcgtgcagcagaga.....ggtgatcaataatcgtagc 2742

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_esc1: \*  
2: gb\_esc2: \*  
3: gb\_hic: \*  
4: gb\_esc3: \*  
5: gb\_esc4: \*  
6: gb\_esc5: \*  
7: gb\_esc6: \*  
8: gb\_gsa1: \*  
9: gb\_gsa2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043	38.0	2829	3 AK004990	AK004990 Mus muscu
2	728	26.5	822	4 BG386074	BG386074 602455248
3	693	25.3	693	9 AY400251	AY400251 Homo sapi
4	686.8	25.0	945	2 BE513091	BE513091 601171545
5	676.4	24.7	693	9 AY400252	AY400252 Pan trogl
6	643	23.5	680	2 BE304667	BE304667 601105783
7	639	23.3	662	4 BM791379	BM791379 K-EST0071
8	637.4	23.2	728	4 BG325755	BG325755 602424466
9	617	22.5	978	4 BG164062	BG164062 602341087
10	614.6	22.4	652	7 CR628947	CR628947 DKF2P469L
11	614.4	22.4	786	8 BZ215522	BZ215522 CH230-416
12	613.6	22.4	650	7 CR546700	CR546700 DKF2P470L
13	606	22.1	643	4 BG328625	BG328625 602427889
14	592	21.6	761	5 BP445902	BP445902 BP445902
15	590.4	21.5	729	7 CN793010	CN793010 4127966 B
16	582.4	21.2	707	7 CK836649	CK836649 4061487 B
17	582.4	21.2	589	2 BU071883	BU071883 im35d1.Y
18	577	21.0	676	2 AM385836	AM385836 CM3-LT004
19	575.6	20.7	630	2 AM837727	AM837727 CM1-LT004
20	566.6	20.7	1043	4 BG164241	BG164241 602341250
21	561	20.5	685	7 CK975368	CK975368 4106492 B
22	555.4	20.3	623	2 AM837724	AM837724 CM1-LT004
23	555	20.2	555	5 BU073403	BU073403 im35d1.x
24	551.6	20.1	727	4 B1101652	B1101652 602887470

25	551.2	20.1	777	4 B1102100	B1102100 602887847
26	550.6	20.1	693	9 AY400253	AY400253 Mus muscu
27	544.4	19.9	752	2 CB952500	CB952500 AGENCOURT
28	543.4	19.8	557	4 BG399901	BG399901 602441435
29	543	19.8	810	4 BG427780	BG427780 602497154
30	531	19.4	884	6 CA469620	CA469620 AGENCOURT
31	526.6	19.2	648	7 CN788131	CN788131 4122426 B
32	522.2	19.0	750	2 AM475316	AM475316 un64d02.Y
33	521.4	19.0	758	2 B1102679	B1102679 602888236
34	521	19.0	724	4 B1100253	B1100253 602885716
35	513	18.7	848	6 CA469366	CA469366 AGENCOURT
36	512.8	18.7	758	6 CB999779	CB999779 AGENCOURT
37	509.4	18.6	818	6 CA469360	CA469360 AGENCOURT
38	508.8	18.6	570	7 CR628828	CR628828 DKF2P469B
39	508.2	18.5	856	2 BP541534	BP541534 602067906
40	507.6	18.5	886	2 BP032123	BP032123 601559727
41	504.8	18.4	846	2 BF789255	BF789255 602105156
42	504.8	18.4	1114	2 BF789836	BF789836 602105395
43	503	18.3	511	1 AM006504	AM006504 wt05e05.x
44	502.4	18.3	546	2 BF819923	BF819923 MR1-RT002
45	501.2	18.3	774	7 CK031415	CK031415 AGENCOURT

#### ALIGNMENTS

RESULT 1  
AK004990  
LOCUS  
DEFINITION  
AK004990 Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300013G06 product:claudin 2, full insert sequence.  
ACCESSION  
AK004990.1 GI:12836594  
VERSION  
AK004990.1  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
JOURNAL  
99279253  
MEDLINE  
10349636  
PUBMED  
10349636  
REFERENCE  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kohno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL  
20499374  
PUBMED  
11042159  
REFERENCE  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kohno, H., Akiyama, J., Nishii, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Mishiue, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL  
20530913  
PUBMED  
11076861  
REFERENCE  
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
JOURNAL  
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.







## ORIGIN

adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) "

Query Match 26.5%; Score 728; DB 4; Length 822;  
Best Local Similarity 96.3%; Pred. No. 3.8e-197;  
Matches 778; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTGAGGTGTTCAAGAGCAAGA 60  
9 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTGAGGTGTTCAAGAGCAAGA 68  
61 GCTTCAGCTGGAAG 120  
69 GCTTCAGCTGGAAG 128  
121 GGCCTCTTGGCCTCAACTTGTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 180  
129 GGCCTCTTGGCCTCAACTTGTGGGCTACATCTAGAGGCTTCTGGGGCTTTTGGGAC 188  
181 ACTGTTGCCATGCTGCTCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
189 ACTGTTGCCATGCTGCTCCAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248  
241 GAG 300  
249 GAG 308  
301 CACCCAGTGAACATCTATAGCACTTCTGGGCTGCGGCTGACATCCAGGCTGCCCA 360  
309 CACCCAGTGAACATCTATAGCACTTCTGGGCTGCGGCTGACATCCAGGCTGCCCA 368  
361 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
369 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 428  
421 CAG 480  
429 CAG 488  
481 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 540  
489 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 548  
541 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 600  
549 TGAAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 608  
601 AGAGGCTCTTTAATCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 660  
609 AGAGGCTCTTTAATCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTTCA 668  
661 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACTAGATGCTCAAGAGCCA 720  
669 CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACTAGATGCTCAAGAGCCA 727  
721 ACCTCTTTCAGCAAGAGAGCTCTCCAGAGGCTGATCACTCCAAAGTCAAGAGTGA 780  
728 CTC---TTGACAAAGAGAGCTCTCCAGAGGCTGATCACTCCAAAGTCAAGAGTGA 784  
781 CAATTCTTACAGCTGACAGAGATG 808  
785 CCAAT-CTACAGAGCTGACAGAGATG 811

RESULT 3  
AY400251 693 bp DNA linear GSS 15-DEC-2003  
LOCUS Homo sapiens CLDN2 gene, VIRUTAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.

ACCESSION AY400251 GI:39756240  
VERSION GSS.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 693)  
Clair,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
2 (bases 1 to 693)  
Clair,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

COMMENT  
FEATURES  
source  
1..693  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>693  
/gene="CLDN2"  
/locus\_tag="HOMO495"

## ORIGIN

Query Match 25.3%; Score 693; DB 9; Length 693;  
Best Local Similarity 100.0%; Pred. No. 4.2e-187;  
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

119 ATGGCTCTTTGGCTCCAACTTGGGCTAATCTTAGGCTTGGGGCTTTGGGC 178  
1 ATGGCTCTTTGGCTCCAACTTGGGCTAATCTTAGGCTTGGGGCTTTGGGC 60  
179 ACACTGTTGCATGCTGCTCCAGCTGGAAGAAAGATTCTTATGCGTGCAGATT 238  
61 ACATGTTGCATGCTGCTCCAGCTGGAAGAAAGATTCTTATGCGTGCAGATT 120  
239 GTGACAGAGTGGCTTCTCAAGAGGCTCTGATGATGATGATGATGATGATGATG 298  
121 GTGACAGAGTGGCTTCTCAAGAGGCTCTGATGATGATGATGATGATGATGATG 180  
299 ATCAACCAAGTGTGACATCTATAGCACTTCTGGGCTGCGGCTGACATCCAGGCTGCC 358  
181 ATCAACCAAGTGTGACATCTATAGCACTTCTGGGCTGCGGCTGACATCCAGGCTGCC 240  
359 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 418  
241 CAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
419 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 478  
301 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
479 GGTGAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTT 538  
361 GGTGAGTCTTTTCACTCTTGAAGGCTCTGAGGATCATCTGTTCTGAGATCTT 420  
539 CATGAGTCTTACAGGAGCTTCTACTACACAGCTGATGATGATGATGATGATGATG 598  
421 CATGAGTCTTACAGGAGCTTCTACTACACAGCTGATGATGATGATGATGATGATG 480  
599 GAGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATGATGATGATG 658

Db 481 GGAGAGGCTCTTACTGAGGCAATATTTCTTCCCTGTTCCCTGATAGCTGAATCATC 540  
 Qy 659 CTCTGCTTTTCCCTGCTATATCCAGAGAAATGCTCCCAACTACTACTGCTTACCAAGCC 718  
 Db 541 CTCTGCTTTTCCCTGCTATATCCAGAGAAATGCTCCCAACTACTACTGCTTACCAAGCC 600  
 Qy 719 CAACCTCTTGCACAAGAGGCTCTCCAAAGGCTGCTCAACCTCCCAAGTCAAGAGTGA 778  
 Db 601 CAACCTTTTCCACAGAGAGCTCTCCAAAGGCTGCTCAACCTCCCAAGTCAAGAGTGA 660  
 Qy 779 TTCAATTCCTACAGCCTGACAGGGTATGTGTA 811  
 Db 661 TTCAATTCCTACAGCCTGACAGGGTATGTGTA 693

RESULT 4  
 BES13091 945 bp mRNA linear EST 07-AUG-2000  
 LOCUS 601171545F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:3545171 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BES13091  
 VERSION BES13091.1 GI:9720302  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 945)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: egsb@remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov  
 Plate: L10M241 row: 1 column: 12  
 High quality sequence start: 36  
 High quality sequence stop: 782.  
 Location/Qualifiers  
 1. 945  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3545171"  
 /issue\_type="adenocarcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_15"  
 /note="Organ: colon; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN  
 Query Match 25.0%; Score 686.8; DB 2; Length 945;  
 Best Local Similarity 94.0%; Pred. No. 2.8e-185;  
 Matches 758; Conservative 0; Mismatches 42; Indels 6; Gaps 4;

Qy 1 AGAAGTCAGCTGCGACAGAGACTCTGAATGAGGATTAGAGGTTTCAAGAGCAGAGA 60  
 Db 69 AGAAGTCAGCTGCGACAGAGACTCTGAATGAGGATTAGAGGTTTCAAGAGCAGAGA 128  
 Qy 61 GCTTCAGCTCGAAGACAGAGGAGGAGTCCCTGAAGAGCCTTCTAAGAGGCTTGCAT 120  
 Db 129 GCTTCAGCTCGAAGACAGAGGAGGAGTCCCTGAAGAGCCTTCTAAGAGGCTTGCAT 188

Qy 121 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCA 180  
 Db 189 GGCCTCTTGGGCTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCA 248  
 Qy 181 ACTGTTGCCATGCTCTCCAGCTGAGAAACAACTTCTTATGTGCTGCTGAGATTT 240  
 Db 249 ACTGTTGCCATGCTCTCCAGCTGAGAAACAACTTCTTATGTGCTGCTGAGATTT 308  
 Qy 241 GACAGAGTTGGCTTCTCCAAAGGCTCTGGAATGGAATGTCACACAGCAAGGCAT 300  
 Db 309 GACAGAGTTGGCTTCTCCAAAGGCTCTGGAATGGAATGTCACACAGCAAGGCAT 368  
 Qy 301 CACCCAGTGTGATCTATAGCACCTTCTGGGCTGCGGCTGATCATCCAGGCTGCCA 360  
 Db 369 CACCCAGTGTGATCTATAGCACCTTCTGGGCTGCGGCTGATCATCCAGGCTGCCA 428  
 Qy 361 GGCATGATGTGATGATCCAGTGCAATCTCTCCCTGAGCTGATATCTGTGGTGG 420  
 Db 429 GGCATGATGTGATGATCCAGTGCAATCTCTCCCTGAGCTGATATCTGTGGTGG 488  
 Qy 421 CATGAGATGACAGTCTTCTGCCAGGAATCCGACCAAGACAGAGTGGCGGTACAG 480  
 Db 489 CATGAGATGACAGTCTTCTGCCAGGAATCCGACCAAGACAGAGTGGCGGTACAG 548  
 Qy 481 TGGAGTCTTTTTCATCTGAGAGGCTCTGGGATCATTCCTGTTGCTGGAATCTTCA 540  
 Db 549 TGGAGTCTTTTTCATCTGAGAGGCTCTGGGATCATTCCTGTTGCTGGAATCTTCA 607  
 Qy 541 TGGAGTCTTACGAGGACTTCTACTACCACTGATGCTGACAGCATGAATTTGA--GATT 598  
 Db 608 TGGAGTCTTACGAGGACTTCTACTACCACTGATGCTGACAGCATGAATTTGA--GATT 667  
 Qy 599 GAGAGGCTTTTACTTGGGCAATATTTCTCCCTGTTCTCCCTGATAGTGAATCA--T 657  
 Db 668 GAGAGGCTTTTACTTGGGCAATATTTCTCCCTGTTCTCCCTGATAGTGAATCA--T 727  
 Qy 658 CCTGTGTTTCTGCTCATCCAGAAATGCTCCAACTACTAGATGCTTACCAAGC 717  
 Db 728 CCTGTGTTTCTGCTCATCCAGAAATGCTCCAACTACTAGATGCTTACCAAGC 787  
 Qy 718 CCAACTCTTGCACAAGAGCTCTCCAAAGCTGTCAACTCCCAAGTCAAGGTGA 777  
 Db 788 CGCACCTCTTGCACAAGAGCTCTCCAAAGCTGTGTGATCCTTCCAAAGTCAAGGT-- 845  
 Qy 778 GTTCAATTCCTACAGCTTACAGGCT 803  
 Db 846 GTTCAATTCCTACAGCTTACAGGCT 871

RESULT 5  
 AY400252 693 bp DNA linear GSS 15-DEC-2003  
 LOCUS Pan troglodytes C12N2 gene, VIRUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AY400252  
 VERSION AY400252.1 GI:39756241  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.  
 REFERENCE 1 (bases 1 to 693)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
 Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 693)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

FEATURES	COMMENT
Location/Qualifiers	This sequence was made by sequencing genomic exons and ordering them based on alignment.

gene

## ORIGIN

Query Match	24.7%	Score 676.4	DB 9	Length 693
Best Local Similarity	97.7%	Pred. No. 2.5e-182		
Matches 677	Conservative 0	Mismatches 16	Indels 0	Gaps 0

QY	119	ATGACCCTCTTGGAGCTCAACTTGTGGGCTAATCTAGAGCCTTCTGGAGCTTTTGGAGC	178
Db	1	ATGGCTCTCTTGGGCTCCAACTGTGTGNNNNMATTMTATNNCCNNNNNGGGCTTTTGGGC	60
QY	179	ACACTGTGTGCATGCTGCTGCCAGCTGGAAAACAAGTTCTTATGTGTGGTSCAGCAATT	238
Db	61	ACNNATGTGTGGCAATGCTGCTGCCAGCTGGAAAACAAGTTCTTATGTGTGGTSCAGCAATT	120
QY	239	GTCACAGACAGTGGGCTTCCAGAGGAGCTCTGAGATGAAATGTGCACACACAGCACAGGC	298
Db	121	GTGACAGACAGTGGGCTTCTCCAGAGGAGCTCTGTGATGAAATGTGCACACACAGCACAGGC	180
QY	299	ATCACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGTGCCGTGACATCCAGGCTGCC	358
Db	181	ATCACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGTGCCGTGACATCCAGGCTGCC	240
QY	359	CAGGCGCATGATGGTGAACATCCAGTGCATCTCTCCGAGGCTGTGATTAATCTGTGGTGTG	418
Db	241	CAGGCGCATGATGGTGAACATCCAGTGCATCTCTCCGAGGCTGTGATTAATCTGTGGTGTG	300
QY	419	GGCATGAGATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCA	478
Db	301	GGCATGAGATGCACAGTCTTCTGCCAGGAATCCGAGCCAAAGACAGAGTGGCGGTAGCA	360
QY	479	GGTGGAGTCTTTTTCATCTCTTGGAGGCTCTCTGGGATTCATTCTCTGTGTGCTTGAATCTT	538
Db	361	GGTGGAGTCTTTTTCATCTCTTGGAGGCTCTCTGGGATTCATTCTCTGTGTGCTTGAATCTT	420
QY	539	CATGGAGTCTCCACGGGACTTCTACTCACCACTGTGCTGTGACAGCATGAAATTTGAGATT	598
Db	421	CATGGAGTCTCCACGGGACTTCTACTCACCACTGTGCTGTGACAGCATGAAATTTGAGATT	480
QY	599	GGAGAGGCTCTTATCTTGTGGCAATATTTCTTCCGTTCCTCTGTATAGCTGGAATCATC	658
Db	481	GGAGAGGCTCTTATCTTGTGGCAATATTTCTTCCGTTCCTCTGTATAGCTGGAATCATC	540
QY	659	CTCTGCTTTTCTGTCTCATCTCCAGAGGAATGTGCTCAACTGATAGAGCTCAACCAAGCC	718
Db	541	CTCTGCTTTTCTGTCTCATCTCCAGAGGAATGTGCTCAACTGATAGAGCTCAACCAAGCC	600
QY	719	CAACCTCTTGGCACAGAGAGCTTTCAGAGGCTGTGTCAACTCTCCAAAGTCAAGATGAG	778
Db	601	CAACCTCTTGGCACAGAGAGCTTTCAGAGGCTGTGTCAACTCTCCAAAGTCAAGATGAG	660
QY	779	TTCAATTCTTACAGCTGTGACAGGGATGTGTGGA 811	
Db	661	TTCAATTCTTACAGCTGTGACAGGGATGTGTGGA 693	

RESULT 6  
BE304667

LOCUS	BE304667	680 bp	mRNA	linear	EST 13-JUL-2000
DEFINITION	61105783.F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:2988309 5',				
ACCESSION	mRNA sequence.				
VERSION	BE304667				
KEYWORDS	BE304667.1	GI:9176036			
SOURCE	EST.				
ORGANISM	Homo sapiens	(human)			
	Homo sapiens				

FEATURES	Location/Qualifiers
source	1. .680

## ORIGIN

Query Match 23.5%; Score 643; DB 2; Length 680;  
Best Local Similarity 100.0%; Pred. No. 9.7e-173;  
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	224	GTGGGTGTCAGCAATTGTGACAGCAGTTGGCTTTCTCCAAAGGACCTCTGGATGTGAATGTGACC	283
Db	38	GTGGGTGTCAGCAATTGTGACAGCAGTTGGCTTTCTCCAAAGGACCTCTGGATGTGAATGTGATGCC	97
Qy	284	ACAACAAGCA CAGGCATCAACCAAGTGTGACATCTATAGAACCTTCTGGGCTTGCCGCT	343
Db	98	ACAACAAGCA CAGGCATCAACCAAGTGTGACATCTATAGAACCTTCTGGGCTTGCCGCT	157
Qy	344	GACATCCAGGCTGCCCCAGGCCATGATGTGTGACATCCAGTGCATCTCTCTCCCTGGCCTGAC	403
Db	158	GACATCCAGGCTGCCCCAGGCCATGATGTGTGACATCCAGTGCATCTCTCTCCCTGGCCTGAC	217
Qy	404	ATTATCTCTGTGTGGGCGCATGAGATGACAGTCTTTCGCCAGGAATCCGAGCCAAAGAC	463
Db	218	ATTATCTCTGTGTGGGCGCATGAGATGACAGTCTTTCGCCAGGAATCCGAGCCAAAGAC	277
Qy	464	AGAAGTGCAGGTAGCAGGTGAGTCTTTTTCATCCTTTGGAGGACCTCTGGGATTCATTTCT	523
Db	278	AGAAGTGCAGGTAGCAGGTGAGTCTTTTTCATCCTTTGGAGGACCTCTGGGATTCATTTCT	337
Qy	524	GTTCGCTGGAATCTTCAATGGGATCTCAACGGGACTTCACTCAACCACTGTGGCTCGACAGC	583
Db	338	GTTCGCTGGAATCTTCAATGGGATCTTCAACGGGACTTCACTCAACCACTGTGGCTCGACAGC	397
Qy	584	ATGAAATTTGAGATTGGACAGGCTCTTTTACTTGGGCAATTATTTCTTCCCTGTTCTCCCTG	643

|||||  
Db ATGAATTGAGATGAGAGGCTTTTACTTGGGATTTATTTCTCCGTCTCCCTG 457  
QY 644 ATAGCTGGATCATCTCTGCTTTTCTGCTCATCCAGAGAAATGCTCACTACTAC 703  
Db 458 ATAGCTGGATCATCTCTGCTTTTCTGCTCATCCAGAGAAATGCTCACTACTAC 517  
QY 704 GATGCTCAAGAGCCCAAGCTTTGCAAGAGAGCTCTCAAGAGCTGCTCACTCTCC 763  
Db 518 GATGCTCAAGAGCCCAAGCTTTGCAAGAGAGCTCTCAAGAGCTGCTCACTCTCC 577  
QY 764 AAGTCAAGAGTGAATTCCTTCAAGAGCTGCAAGAGTATGTGAAGAACAGAGGAGC 823  
Db 578 AAGTCAAGAGTGAATTCCTTCAAGAGCTGCAAGAGTATGTGAAGAACAGAGGAGC 637  
QY 824 CAGAGCTGGGGGGTGGCTGGCTGTGTGAAAACAGTGGACAGC 866  
Db 638 CAGAGCTGGGGGGTGGCTGGCTGTGTGAAAACAGTGGACAGC 680

RESULT 7  
BM791379 662 bp mRNA linear EST 05-MAR-2002  
LOCUS K-EST0071366 S21SNUS20 Homo sapiens cDNA clone S21SNUS20-14-C06 5',  
DEFINITION mRNA sequence.  
BM791379  
ACCESSION BM791379.1 GI:19139611  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 662)  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongseung@mail.kribb.re.kr  
Plate: 14 row: C column: 06  
High quality sequence stop: 662.  
Location/Qualifiers

## FEATURES

source  
1. 662  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone\_id="S21SNUS20-14-C06"  
/sex="F"  
/tissue\_type="Stomach"  
/cell\_type="Picoating aggregates"  
/cell\_line="SMU-520"  
/lab\_host="Top10"  
/clone\_id="S21SNUS20"  
/note="Organ: Stomach; Vector: pTZ189P1; Site 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tabacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10' by electroporation method.

ORIGIN  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

Query Match 23.3%; Score 639; DB 4; Length 662;  
Best Local Similarity 99.7%; Pred. No. 1,4e-171;  
Matches 661; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1685 TAGGGACCTGACCTGGGCTCTGCTTAAACCAAGGCTAAGGGCTATAGCATGGTT 1744  
Db 1 TAGGGACCTGACCTGGGCTCTGCTTAAACCAAGGCTAAGGGCTATAGCATGGTT 60  
QY 1745 TCCTTAGGAACAGTAAACAGATTTTCTAGAGATGGCCCTTGGCTGGGGATGACATGT 1804  
Db 61 TCCTTAGGAACAGTAAACAGATTTTCTAGAGATGGCCCTTGGCTGGGGATGACATGT 120  
QY 1805 GGGAGCTGGGGGTACTAGAGAAAGACCACTTCTTGAAGGTCTTAAGAGCAGAGTGG 1864  
Db 121 GGGAGCTGGGGGTACTAGAGAAAGACCACTTCTTGAAGGTCTTAAGAGCAGAGTGG 180  
QY 1865 ATGTGTGTGGTGGCTCAAGTGGGTGTTTCTACTCTGCAAGTGAAGAGAGCCCTAGAA 1924  
Db 181 ATGTGTGTGGTGGCTCAAGTGGGTGTTTCTACTCTGCAAGTGAAGAGAGCCCTAGAA 240  
QY 1925 ACTCTTCAGGCGTAAATGAAGAAATCAGCTCAATGATGAGTCAAGGCCCTCCAGGTCCACC 1984  
Db 241 ACTCTTCAGGCGTAAATGAAGAAATCAGCTCAATGATGAGTCAAGGCCCTCCAGGTCCACC 300  
QY 1985 ACAAGACATACAGAGGCTCTGAAAGACATAGCACCAAGCCGCTTCAATTCGCC 2044  
Db 301 ACAAGACATACAGAGGCTCTGAAAGACATAGCACCAAGCCGCTTCAATTCGCC 360  
QY 2045 CACTGTCCATCGGAAGATGTCCAGAGTGGCTTGAAGGGCATTAAGGGCTCCAGCATGGC 2104  
Db 361 CACTGTCCATCGGAAGATGTCCAGAGTGGCTTGAAGGGCATTAAGGGCTCCAGCATGGC 420  
QY 2105 ATATCCATGCCACGAGTGTCTGTCCATGATCTGATGATAGTGCATGCTCTGGGA 2164  
Db 421 ATATCCATGCCACGAGTGTCTGTCTGTCCATGATCTGATGATAGTGCATGCTCTGGGA 480  
QY 2165 TTGACGCTGAGTGGAGTGAAGATGTTCCAGAGACAGTTCACCTTAAGTTC 2224  
Db 481 TTGACGCTGAGTGGAGTGAAGATGTTCCAGAGACAGTTCACCTTAAGTTC 540  
QY 2225 GAAATGTTCCCTTACCCTGAGTGGAGT -GAGGGGTATACACAAAGTATTTTC 2283  
Db 541 GAAATGTTCCCTTACCCTGAGTGGAGTGAAGGGGTATACACAAAGTATTTTC 600  
QY 2284 CTCACAGCTTAGGACATGATGCTGCTTGAAGAAATTCACAGACACCTCTGAACCTCAT 2343  
Db 601 CTCACAGCTTAGGACATGATGCTGCTTGAAGAAATTCACAGACACCTCTCTGAACCTCAT 659  
QY 2344 TGT 2346  
Db 660 TGT 662  
RESULT 8  
BG325755 728 bp mRNA linear EST 27-FEB-2001  
LOCUS BG325755 602424466F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4562273 5',  
DEFINITION mRNA sequence.  
ACCESSION BG325755.1 GI:13132179  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 728)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)











Db 20 AGAAGTCAGCTGGCAGAGAGACTCTGAAATGAGGATTAAGGTGTTCAAGAGCAAGA 79  
Qy 61 GCTTCAAGCTGAAAGCAAGGAGCAAGTCCCTGAAAGAGCTTTCTACTAGAGGTCTGCAT 120  
Db 80 GCTTCAAGCTGAAAGCAAGGAGCAAGTCCCTGAAAGAGCTTTCTACTAGAGGTCTGCAT 138  
Qy 121 GAGCTCTCTGGGCTCCAACTGTGGGCTCATCTAGAGGCTTTGGGGCTTTTGGGAC 180  
Db 139 GAGCTCTCTGGGCTCCAACTGTGGGCTCATCTAGAGGCTTTGGGGCTTTTGGGAC 198  
Qy 181 ACTGTTGCATGCTGCTCCCAAGCTGAAACAAAGTTCTTAATGCTGCTGCAAGCTTGT 240  
Db 199 ACTGTTGCATGCTGCTCCCAAGCTGAAACAAAGTTCTTAATGCTGCTGCAAGCTTGT 258  
Qy 241 GACAGCAGTTGGCTTCTCCAAAGGCTCTGAGTGAATGTCACACACACAGCAGCAT 300  
Db 259 GACAGCAGTTGGCTTCTCCAAAGGCTCTGAGTGAATGTCACACACAGCAGCAT 318  
Qy 301 CACCCAGTGAACATCTATAGCAACCTTGGGCTGTCGCGCTGACATCCAGGCTGCCA 360  
Db 319 CACCCAGTGAACATCTATAGCAACCTTGGGCTGTCGCGCTGACATCCAGGCTGCCA 378  
Qy 361 GGCATGATGCTGATCATCCAGTGAATCTCTCCCTGCTGCTGATATCTCTGTGTGG 420  
Db 379 GGCATGATGCTGATCATCCAGTGAATCTCTCCCTGCTGCTGATATCTCTGTGTGG 438  
Qy 421 CATGATGTCACAGTCTTCTGCGCAGAAATCCGAGCCAAAGACAGAGTGGCGTAGAG 480  
Db 439 CATGATGTCACAGTCTTCTGCGCAGAAATCCGAGCCAAAGACAGAGTGGCGTAGAG 498  
Qy 481 TGAGATCTTTTCACTCTGAGAGGCTCTGAGGATTAATCTCTGCTGCTGAAATCTTCA 540  
Db 499 TGAGATCTTTTCACTCTGAGAGGCTCTGAGGATTAATCTCTGCTGCTGAAATCTTCA 558  
Qy 541 TGAGATCTTACGGGACTTCTACTACCACTGCTGCTGCTGACAGATGAATTTGAGATTGG 600  
Db 559 TGAGATCTTACGGGACTTCTACTACCACTGCTGCTGCTGACAGATGAATTTGAGATTGG 618  
Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTCTTCCC 632  
Db 619 AGAGGCTCTTACTTGGGCAATTAATTTCTTCCC 650

RESULT 13  
BG328625 643 bp mRNA linear EST 27-FBB-2001  
LOCUS 602427889F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4547230 5',  
DEFINITION mRNA sequence.  
ACCESSION BG328625  
VERSION BG328625.1 GI:13135063  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 643)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Straube, Ph.D.  
Email: rstraube@nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
http://image.liml.gov  
Plate: LIML235 row: a column: 23  
High quality sequence stop: 641.  
Location/Qualifiers  
1. 643  
/organism="Homo sapiens"

/mol type="mRNA"  
/db xref="taxon:9606"  
/clone="IMAGE:4547230"  
/issue="adenocarcinoma cell line"  
/lab\_host="PH10B (phage-resistant)"  
/clone\_lib="NIH MGC 15"  
/note="Organ: colon; Vector: pOTB7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the Laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 22.1%; Score 606; DB 4; Length 643;  
Best Local Similarity 99.5%; Pred. No. 4.1e-162;  
Matches 639; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Qy 5 GTGAGCTGGCAAGAGACTCTGAAATGAGGATTAAGGTGTTCAAGAGCAAGCTT 64  
Db 2 GTGAGCTGGCAAGAGACTCTGAAATGAGGATTAAGGTGTTCAAGAGCAAGCTT 61  
Qy 65 CAGCTGAAGACAAGGAGAGAGTCCCTGAAGAGCTTCTACTAGAGGTCTGCATGGCC 124  
Db 62 CAGCTGAAGACAAGGAGAGAGTCCCTGAAGAGCTTCTACTAGAGGTCTGCATGGCC 121  
Qy 125 TCTCTGGCTCCCACTGTGGCTCAATCTAGGCTTCTGAGGCTTTTGGGCAACTG 184  
Db 122 TCTCTGGCTCCCACTGTGGCTCAATCTAGGCTTCTGAGGCTTTTGGGCAACTG 181  
Qy 185 GTTGGCAAGTCTGCTCCCAAGTGAAGAAACAAAGTTCTTAATGCTGCTGCAAG 243  
Db 182 GTTGGCAAGTCTGCTCCCAAGTGAAGAAACAAAGTTCTTAATGCTGCTGCAAG 241  
Qy 244 AGAGTTGGCTTCCCAAGGAGCTCTGAGTGAATGAGGACA -CACAGACAGGATCA 302  
Db 242 AGAGTTGGCTTCCCAAGGAGCTCTGAGTGAATGAGGAGATGTCACACAGACAGGATCA 301  
Qy 303 CCGAGTGTGACATCTATAGCAACCTTCTGAGGCTGCGGCTGACATCCAGGCTGCCAGG 362  
Db 302 CCGAGTGTGACATCTATAGCAACCTTCTGAGGCTGCGGCTGACATCCAGGCTGCCAGG 361  
Qy 363 CCAATGATGTGACATCCAGTGCATCTCTCTGCTGCTGCTGCA -TTATCTCTGTGGGCT 421  
Db 362 CCAATGATGTGACATCCAGTGCATCTCTCTGCTGCTGCTGCA -TTATCTCTGTGGGCT 421  
Qy 422 ATGAGATGACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCAGGT 481  
Db 422 ATGAGATGACAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGAGTGGCGTAGCAGGT 481  
Qy 482 GGAATCTTTTCACTCTTGGAGGCTCTCTGAGATTCATCTCTGTGCTGGAATCTTTCAT 541  
Db 482 GGAATCTTTTCACTCTTGGAGGCTCTCTGAGATTCATCTCTGTGCTGGAATCTTTCAT 541  
Qy 542 GGAATCTTACGGGACTTCTACTACCACTGCTGCTGACAGCATGAATTTGAGATTGGA 601  
Db 542 GGAATCTTACGGGACTTCTACTACCACTGCTGCTGACAGCATGAATTTGAGATTGGA 601  
Qy 602 GAGGCTCTTACTTGGGCAATTAATTTCTGCTGCTGCTGCTG 643  
Db 602 GAGGCTCTTACTTGGGCAATTAATTTCTGCTGCTGCTGCTG 643

RESULT 14  
BP445902 761 bp mRNA linear EST 30-DEC-2003  
LOCUS BP445902  
DEFINITION scrofa cDNA clone LVR010047F07 5', mRNA sequence.  
ACCESSION BP445902  
VERSION BP445902.1 GI:40435969  
KEYWORDS EST.

SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 761)  
 AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,  
 Okumura,N., Hamashima,N. and Awata,T.  
 TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs  
 JOURNAL derived from porcine full-length cDNA libraries  
 COMMENT Nucleic Acids Res. 32 (1), D484-D488 (2004)  
 Contact: Hirohide Uenishi  
 Animal Genome Laboratory, Genome Research Department  
 National Institute of Agrobiological Sciences  
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
 Tel: +81-29-838-8627  
 Fax: +81-29-838-8627  
 Email: huenishi@affrc.go.jp  
 EST project with full-length enriched cDNA libraries carried out in  
 Animal Genome Research Program (Japan) by National Institute of  
 Agrobiological Sciences and STAP-Institute  
 Single pass sequencing of clones derived from oligo-capped cDNA  
 library  
 Vector sequences were eliminated by RepeatMasker version 2002/07/13  
 and crossmatch version 0.990319  
 Low quality bases were trimmed based on the quality values.  
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 /db\_xref="taxon:9823"  
 /clone="LVR010047F07"  
 /issue\_type="liver"  
 /dev\_stage="adult"  
 /clone\_lib="full-length enriched swine cDNA library, adult  
 liver"  
 ORIGIN  
 Query Match 21.6%; Score 592; DB 5; Length 761;  
 Best Local Similarity 88.1%; Pred. No. 4.6e-158;  
 Matches 657; Conservative 0; Mismatches 85; Indels 4; Gaps 1;  
 QY 1 AGAAGTCAGGCTTGGAGAGACATCTGAATGAGGATTAGAGTGC---TTCAAGAGC 56  
 DB 16 AGAGTGTGGGCTGGCGGAGACACTGTGCAATGAGGATTAGAGGCCAGATCCAAAGAGC 75  
 QY 57 AAGAGCTTACGCTGAAGACAAGGAGCAGATCCCTTGAAGACGCTTCTACTGAGAGTCTG 116  
 DB 76 AAGTGTCTACAGCGGAGAGAGAGGAGACGGGCCCTTGAAGACGATCTACGAGAGGTCGG 135  
 QY 117 CCATGGCTCTCTTGGGCTTCAACTGTGAGCTTACATCTTACGCTTCTGAGGCTTTTGG 176  
 DB 136 CCATGGCTCTCTGAGCTTCAACTGTGAGCTTACATCTTACGCTTCTGAGGCTTTTGG 195  
 QY 177 GCACACGTGTTCAGTCTGCTCCCGAGCTGGAAAAAAGATTCTTATGTCGGTCCAGCA 236  
 DB 196 GCACCCCTGTGTCAGTCTGCTCCCGAGCTGGCAAGAGTCTTACGTCGGGCCAGCA 255  
 QY 237 TTGTGACAGAGTGTGCTTCTCCAAAGGGCTCTGATGATGATGACACAGACAGCAG 296  
 DB 256 TCGTGAAGGAGTGTGCTTCTCCAAAGGGCTCTGATGATGATGACACAGACAGCAGC 315  
 QY 297 GCATACCCAGTGTGATCTTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTG 356  
 DB 316 GCATACCCAGTGTGATCTTATGACACCTTCTGGGCTGCGCGCTGACATCCAGGCTG 375  
 QY 357 CCCAAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 416  
 DB 376 CCCAAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 435  
 QY 417 TGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 476  
 DB 436 TGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 495

QY 477 CAGGTGAGTCTTTTCAATCTCTGAGAGGCTCTGAGGATTCATCTGTTGCTGGAATC 536  
 DB 496 TGGGTGAGTCTTTTCAATCTCTGAGAGGCTCTGAGGATTCATCTGTTGCTGGAATC 555  
 QY 537 TTGATGAGTCTTCAAGGAGCTTCTACACCACTGATGATGATGATGATGATGATGATG 596  
 DB 556 TTGATGAGTCTTCAAGGAGCTTCTACACCACTGATGATGATGATGATGATGATGATG 615  
 QY 597 TTGAGAGGCTCTTCAATCTGAGGATTCATCTGATGATGATGATGATGATGATGATG 656  
 DB 616 TGGGAGGCTCTTCAATCTGAGGATTCATCTGATGATGATGATGATGATGATGATG 675  
 QY 657 TCTCTGCTTTTCTGCTATCCAGAGATGCTTCAATCTGATGATGATGATGATGATG 716  
 DB 676 TCTCTGCTTTTCTGCTATCCAGAGATGCTTCAATCTGATGATGATGATGATGATG 735

RESULT 15  
 LOCUS CN793010 729 bp mRNA linear EST 26-MAY-2004  
 DEFINITION 4127966 BARC 8BOV Bos taurus cDNA clone 8BOV\_46D02 5', mRNA  
 sequence.  
 ACCESSION CN793010  
 VERSION CN793010.1 GI:47688990  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 729)  
 REFERENCE Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and  
 Matukumalli,L.K.  
 TITLE Construction and Analysis of a cDNA Library Generated From  
 JOURNAL Intestinal Muscle and Epithelial Tissues of Holstein Cattle  
 COMMENT Unpublished (2004)  
 Contact: Richard G. Baumann  
 Bovine Functional Genomics Lab  
 ANRI  
 BLDG 162; BARC-EAST, Beltsville, MD 20705, USA  
 Tel: 3015048604  
 Fax: 3015048744  
 Email: rbaumann@anri.barc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 0.000925 using options -trimalt - -trim faaltvector identified by  
 cross\_match using options -mismatch 12 -minscore 12  
 Plate: 46 row: D column: 02  
 Seq primer: CCATATTAGGTGACACTATGAGAAC  
 High quality sequence stop: 729.  
 Location/Qualifiers  
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 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Holstein"  
 /db\_xref="taxon:9913"  
 /clone="8BOV\_46D02"  
 /sex="Female"  
 /tissue\_type="Epithelial, Muscle"  
 /dev\_stage="Lactating, Neonatal"  
 /lab\_host="PH108 Tona"  
 /clone\_lib="BARC 8BOV"  
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:  
 NCI; Site 2: SCOR1; Normalized cow cDNA intestinal  
 library in pCMVSPORT6.1, constructed from equimolar mRNA  
 pools derived from 5 sources; 4 lactating intestinal, 1  
 neonatal intestinal 4/5 lactating, proximal duodenum,  
 jejunum, distal ileum, colon, 1/5 neonatal, proximal  
 duodenum, jejunum, distal ileum"

ORIGIN





GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 08:29:24 ; Search time 18345 Seconds  
(Without alignments)  
7068.321 Million cell updates/sec

Title: US-09-787-677A-7  
Perfect score: 2742  
Sequence: 1 agagagcagccgcgcagaga.....gtcgtacataatcgtagc 2742

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 20

Total number of hits satisfying chosen parameters: 1629

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

## Post-processing: Listing first 45 summaries

## Database :

GenBml:.\*  
1: gb da:.\*  
2: gb htg:.\*  
3: gb\_in:.\*  
4: gb\_cm:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
9: gb\_pr:.\*  
10: gb\_ro:.\*  
11: gb\_sts:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2742	100.0	2742	6 BD237562	BD237562 Membrane-
2	2717	99.1	2959	9 AK075405	AK075405 Homo sapi
3	2717	99.1	109465	9 AL158821	AL158821 Human DNA
4	2513	91.6	2863	6 AX136129	AX136129 Sequence
5	2513	91.6	2863	6 BD123517	BD123517 Secretory
6	2513	91.6	2863	9 AK075371	AK075371 Homo sapi
7	1472	53.7	1475	6 AX092348	AX092348 Sequence
8	1472	53.7	1475	6 AX299996	AX299996 Sequence
9	1472	53.7	1475	6 AX395213	AX395213 Sequence
10	1472	53.7	1475	6 AX454606	AX454606 Sequence
11	1472	53.7	1475	6 AX464358	AX464358 Sequence
12	1472	53.7	1475	6 AX491084	AX491084 Sequence
13	1472	53.7	1475	6 AX697065	AX697065 Sequence
14	1472	53.7	1475	6 AY358474	AY358474 Homo sapi
15	1470	53.6	1506	9 BC014424	BC014424 Homo sapi
16	1470	53.6	1918	9 AF177340	AF177340 Homo sapi
17	1291	47.1	1400	6 AK340765	AK340765 Sequence
18	1291	47.1	1400	6 BD085944	BD085944 Elongatio
19	964	35.2	1441	6 AX286822	AX286822 Sequence

20	935	34.1	1618	9 BC071747	BC071747 Homo sapi
21	896	32.7	1524	6 AR340718	AR340718 Sequence
22	896	32.7	1524	6 BD085897	BD085897 Elongatio
23	693	25.3	693	6 C0732222	C0732222 Sequence
24	693	25.3	693	6 AF250558	AF250558 Homo sapi
25	591	21.6	693	6 AX497200	AX497200 Sequence
26	300	10.9	300	6 BD128818	BD128818 Human gen
27	300	10.9	300	6 AX939252	AX939252 Sequence
28	300	10.9	405	6 BD077679	BD077679 5'EST of
29	269	9.8	405	6 AX329986	AX329986 Sequence
30	253	9.2	615	6 AX136475	AX136475 Sequence
31	253	9.2	615	6 BD123715	BD123715 Secretory
32	235	8.6	285	6 BD128830	BD128830 Human gen
33	227	8.3	324	6 AX939253	AX939253 Sequence
34	227	8.3	324	6 BD077680	BD077680 5'EST of
35	178	6.5	248	6 AX136625	AX136625 Sequence
36	178	6.5	248	6 BD123865	BD123865 Secretory
37	155	5.7	300	6 BD212444	BD212444 Novel hum
38	120	4.4	735	11 BV208439	BV208439 ClDN2_226
39	109	4.0	182	6 AX072760	AX072760 Sequence
40	60	2.2	60	6 C0546553	C0546553 Sequence
41	47	1.7	239385	2 AC109686	AC109686 Rattus no
42	47	1.7	250600	2 AC136646	AC136646 Rattus no
43	46	1.7	268828	2 AC091513	AC091513 Rattus no
44	46	1.7	953	4 AF358907	AF358907 Canis fam
45	36	1.3	779	6 AX286824	AX286824 Sequence

## ALIGNMENTS

RESULT 1	BD237562	2742 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD237562				
DEFINITION	Membrane-associated organized protein.				
ACCESSION	BD237562.1	GI:33047332			
VERSION	BD237562.1				
KEYWORDS	JP 2002525113-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Yue,H., Lal,P., Corley,N.C., Guegler,K.J., Baughn,M.R., Lu,A.D. and Tang,T.Y.				
TITLE	Membrane-associated organized proteins				
JOURNAL	Patent: JP 2002525113-A 3 13-AUG-2002;				
COMMENT	INCYTE PHARMACEUTICALS INC				
OS	Homo sapiens (human)				
PN	JP 2002525113-A/3				
PD	13-AUG-2002				
PF	23-SEP-1999 JP 2000572362				
PR	25-SEP-1998 US 60/155215,13-OCT-1998 US 60/155551 PR				
PI	HENRY YUE, PREETI LAL, NEIL C CORLEY, KARL J GUEGLER, MARIAH R BAUGHN,				
PI	AINA D LU, TOM Y TANG				
PC					
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Oca,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,  
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Nakanura,Y., Nagahari,K., Sugano,S. and Isogai,T.  
HRI human cDNA sequencing project  
Unpublished  
2 (bases 1 to 2959)  
Isogai,T. and Yamamoto,J.  
Direct Submission  
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,  
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan  
(E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass  
sequencing, clone selection and full insert sequencing; Helix  
Research Institute (supported by Japan Key Technology Center etc.);

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SOURCE  
ORGANISM

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similar to KIAA0136, a eukaryotic translation elongation factor 1  
alpha 1 (EEF1A1) pseudogene and a CpG island, complete sequence.  
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Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 109465)  
 AUTHORS Heath, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphrey@sanger.ac.uk  
 On Jun 8, 2001 this sequence version replaced gi:1416098.

## COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, Sw, SWISSPROT, Tr, TrEMBL, Wp, WormPep; information on the WormPep database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)

This sequence is not the entire insert of clone RPI-75H8. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPI-75H8 is at 1 in this sequence. The true left end of clone RPI3-383K5 is at 109366 in this sequence.

## FEATURES

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 64..1090  
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 2112..2514  
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## gene

## mRNA

## CDS

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AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
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Helix Research Institute (Jp)
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Db	593	TGAGATCTTTTTCATCTCTGAGAGGCGCTCCTGGGATTCATTCCTGTGTGCTGGAATCTTCA	652
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Oy	1381	CTGAATAATAAACCACTTACGGTATCCAGGGAAAGAAAGCAGATGACAGATGGGAGGA	1440
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Db	1853	GATTTCCTTAAGAAACAGTAACAACAATTTTTCTAAGGATGAGCCCTTGCTGGGAGATGACA	1912
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Db	1913	GTGTGGAGAGCTGTGGGGGTACTGAGGAAAGACACAATTCCTTAAGCGGTGTCTTAAGAACCGAG	1972
QY	1861	GTGGAATGATGTGGGTGGGCTCAGTGGGGGTCTTAATCTCTGSCAGTGAAGGACAGCCCTT	1920
Db	1973	GTGGAATGATGTGGGTGGGCTCAGTGGGGGTCTTAATCTCTGSCAGTGAAGGACAGCCCTT	2032
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Db	2093	ACCACACAGAGCACTACAGAGGCTCTGAAAGACATATGACACCAAGCGAGCCCTTCAATT	2152
QY	2041	CCCCACGTGCATTCGGAAGATGTGCCAGATGGCTTAGAGGGCACTTAAGGGCTCCAGCA	2100
Db	2153	CCCCACGTGCATTCGGAAGATGTGCCAGATGGCTTAGAGGGCACTTAAGGGCTCCAGCA	2212
QY	2101	TGGCATATCCATGAGCCACAGGTGCTGTGTCCATGATCTGAGTGAATGCTGCACTGTGCT	2160
Db	2213	TGGCATATCCATGAGCCACAGGTGCTGTGTCCATGATCTGAGTGAATGCTGCACTGTGCT	2272
QY	2161	GAGATATGACGTGAGGTGGAGTGGAGATGATGTTTCCAGAGAAACAGTTTCACTCTTAAG	2220
Db	2273	GAGATATGACGTGAGGTGGAGTGGAGATGATGTTTCCAGAGAAACAGTTTCACTCTTAAG	2332
QY	2221	GTCCGAAATATGTTCCCTTTAACCTTCGAGATGGGAATGAGGGGTCAATPACCAAAAGTATTT	2280
Db	2333	GTCCGAAATATGTTCCCTTTAACCTTCGAGATGGGAATGAGGGGTCAATPACCAAAAGTATTT	2392
QY	2281	TCCCTCAACAAGCTTAAGCATGATGAGCTTTCTGAAGAAATTTCCAGACACCTTCTCGAACCT	2340
Db	2393	TCCCTCAACAAGCTTAAGCATGATGAGCTTTCTGAAGAAATTTCCAGACACCTTCTCGAACCT	2452
QY	2341	CATTGTCAAGACAGAGAGGCGCCATCTGTTGTCTGTAACATGCTTTTCAATGTCCACTTTC	2400
Db	2453	CATTGTCAAGACAGAGAGGCGCCATCTGTTGTCTGTAACATGCTTTTCAATGTCCACTTTC	2512
QY	2401	TTTGCAATGTTCCAGTGTCTTCCCAACCTGGAAGGCGGTCTCCCTTAAGCAAGTCCCTCC	2460
Db	2513	TTTGCAATGTTCCAGTGTCTTCCCAACCTGGAAGGCGGTCTTCCCTTAAGCAAGTCCCTCC	2572
QY	2461	TCAGGCTTGAGAACTTCTCAGAGGTCACCTCTCTCAATTGAGCTTCTGATCACTTCA	2520
Db	2573	TCAGGCTTGAGAACTTCTCAGAGGTCACCTCTCTCTCAATTGAGCTTCTGATCACTTCA	2632

Qy	2521	TCGCTTCCTCAACCCCTCCCTCCCAACCCCAACCTCAATGTAATTAATGCTCTGAGAGCTAG	2580
Db	2633	TCCTCTCTCAACCCCTCCCTCCCAACCCCAACCTCAATGTAATTAATGCTCTGAGAGCTAG	2632
Qy	2581	CATTCACAATTTTGTATGATCGTATTTGTGTGTGTGTCCGATCTCAAGATATAT	2640
Db	2693	CATTCACAATTTTGTATGATCGTATTTGTGTGTGTGTCCGATCTCAAGATATAT	2752
Qy	2641	GTAACCCCTTGCGTGGTGGGGGGCCATATCTAGACTCTCTGTATCCCAAGACTATCT	2700
Db	2753	GTAACCCCTTGCGTGGTGGGGGGCCATATCTAGACTCTCTGTATCCCAAGACTATCT	2812
Qy	2701	GTAACAGTCCAGGCAC	2717
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LOCUS	BD123517	2863 bp	DNA
DEFINITION	BD123517	2863 bp	linear
ACCESSION	BD123517		
VERSION	BD123517.1		
KEYWORDS	JP 2002017376-A/26.		
SOURCE	JP 2002017376-A/26.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2863)		
TITLE	Ota,T., Iwagai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
JOURNAL	Secretory protein or membrane protein Patent: JP 2002017376-A 26 22-JAN-2002; HELIX RESEARCH INSTITUTE		
COMMENT	OS Homo sapiens (human) PN JP 2002017376-A/26 PD 22-JAN-2002 JP 2000253173 PI 07-JUL-2000 JP 2000253173 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU PI SUGIYAMA, KI KOJI HAYASHI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12P21/08, C12N15/00, C12N5/00 CC Secretory protein or membrane protein FH Key location/Qualifiers (231)..(920). FT CDS location/Qualifiers 1..2863 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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ORIGIN			
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Qy	61	GCTTACGCTGAAGACAAGAGGAGAGTCCCTGAAGAGCTTCTACTAGAGGCTGCAT	120
Db	173	GCTTACGCTGAAGACAAGAGGAGAGTCCCTGAAGAGCTTCTACTAGAGGCTGCAT	232
Qy	121	GGCCTCTCTTGCTCAACTTGTGGGCTACATCTTAGGCTTCTGTGGGCTTTTGGGAC	180
Db	223	GGCCTCTCTTGCTCAACTTGTGTGGGCTACATCTTAGGCTTCTGTGGGCTTTTGGGAC	292
Qy	181	ACTGGTGCATGCTGCTCCCAAGCTGAAAACAAGTTCTTATGTCGCTGCCAGATTGT	240

Db	293	ACTGATGGCCATGCTGCTCCCAAGCTTGATATGTCGGTGCACATTTGT	352
Qy	241	GACGACAGTTGAGCTTCTTCCAAAGGCGCTCTGGATGGAAATGTCGCCACACACGACAGGCAT	300
Db	353	GACGACAGTTGAGCTTCTTCCAAAGGCGCTCTGGATGGAAATGTCGCCACACACGACAGGCAT	412
Qy	301	CACCAAGTGAACATCTATAGCAACCTTCTGGGCGTCGCCGTACATCCAGGCTGCGCA	360
Db	413	CACCAAGTGAACATCTATAGCAACCTTCTGGGCGTCGCCGTACATCCAGGCTGCGCA	472
Qy	361	GGCCATGATGATGATCATCTCAGTGCATCTCCCTCGGCGTCGATTAATCTCTGTGTGGG	420
Db	473	GGCCATGATGATGATCATCTCAGTGCATCTCCCTCGGCGTCGATTAATCTCTGTGTGTGGG	532
Qy	421	CATGATGATGACAGCTCTTCTGCCAGGAATCCCGACCAAGACAGAGTGGCGGTAGCAGG	480
Db	533	CATGATGATGACAGCTCTTCTGCCAGGAATCCCGACCAAGACAGAGTGGCGGTAGCAGG	592
Qy	481	TGGAGTCTTTTATTCCTTGGAGGCGCTCGGGATTAATCTCTGTGCTGGATCTTCA	540
Db	593	TGGAGTCTTTTATTCCTTGGAGGCGCTCGGGATTAATCTCTGTGCTGGATCTTCA	652
Qy	541	TGGATCCCTACGGGACTTCTACACCACTGGTCCCTGACAGACATGAAATTTGAGATTGG	600
Db	653	TGGATCCCTACGGGACTTCTACACCACTGGTCCCTGACAGACATGAAATTTGAGATTGG	712
Qy	601	AGAGGCTCTTTACTTGGGACTTAATTTCTTCCCTGTCTCCCTGATAGCTGAAATCATCT	660
Db	713	AGAGGCTCTTTACTTGGGACTTAATTTCTTCCCTGTCTCCCTGATAGCTGAAATCATCT	772
Qy	661	CTGCTTTTCCGTCATATCCCAAGAAATCGTCCACATACAGATGCTACCAAGGCCA	720
Db	773	CTGCTTTTCCGTCATATCCCAAGAAATCGTCCACATACAGATGCTACCAAGGCCA	832
Qy	721	ACCTCTTGCACAAGAGAGCTCTCCAGGCGCTGTCAAACCTTCCCAAAGTCAAGATGAGTT	780
Db	833	ACCTCTTGCACAAGAGAGCTCTCCAGGCGCTGTCAAACCTTCCCAAAGTCAAGATGAGTT	892
Qy	781	CAATTTCTTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCGACAGCTGGGCGGTGGC	840
Db	893	CAATTTCTTACAGCTGACAGGGTATGTGTGAAGAACAGGGGCGACAGCTGGGCGGTGGC	952
Qy	841	TGGGCTGTGTGAAAAACAGTGCACAGCAACCCGAGGGCCACAGGTGAGGGAACATACCACT	900
Db	953	TGGGCTGTGTGAAAAACAGTGCACAGCAACCCGAGGGCCACAGGTGAGGGAACATACCACT	1012
Qy	901	GAATCGTGTGAAAGGTGCTGCTGAGGATAGACTGACTTTTGGCCATTGGATTGAGCAAG	960
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Qy	1261	TTTGTGTGGGCAATGCTCTAACCTTAACCTTCTCAAGCTCCCTCCAAAGAACTGATTTGGCC	1328
Db	1373	TTTGTGTGGGCAATGCTCTAACCTTCTCAAGCTCCCTCCAAAGAACTGATTTGGCC	1432



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RESULT 6  
AK075371  
LOCUS  
DEFINITION  
Homo sapiens cDNA PSEC0059 fls, clone NT2RP2000601, highly similar  
to Mus musculus claudin-2 mRNA.  
ACCESSION  
AK075371  
VERSION  
AK075371.1 GI:22761413  
KEYWORDS  
oligo capping; fls (full insert sequence).  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,  
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,  
Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.  
HRI human cDNA sequencing project  
Unpublished  
2 (bases 1 to 2863)  
JOURNAL  
Isogai, T. and Yamamoto, J.  
Direct Submision  
Submitted (20-MAR-2002) Takeo Isogai, Helix Research Institute,  
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass  
sequencing, clone selection and full insert sequencing; Helix  
Research Institute (supported by Japan Key Technology Center etc.);  
cDNA library construction; Institute of Medical Science, University  
of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES  
source  
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CDS







QY 1021 CAGCCTTCTGTTTCTCTCACTGCTGCTCCCTGCTTAAGTCCCAACCTCAACTT 1080  
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DB 1084 GAAACCCCAATCCCTTAAGCAGAGACTCAAGAGATCCCTTGGCTCTGCTTAACTGGG 1143  
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QY 1441 CAGGAGGAG 1472  
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AX299996 1475 bp DNA linear PAT 26-NOV-2001  
DEFINITION Sequence 1 from Patent WO0166740.  
ACCESSION AX299996  
VERSION AX299996.1 GI:17129473

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eaton,D.L., Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J.,  
Gurney,A.L., Tumas,D., Matanabe,C.K., Wood,W.I. and Zhang,Z.  
TITLE Compositions and methods for the treatment of immune related  
diseases

JOURNAL Patent: WO 0166740-A 1 13-SEP-2001;  
Genentech, Inc. (US)  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 304 CACCCAG 363  
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DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
QY 481 TGGAGTCTTTCATCTTGGAGGCTCCCTGGAGTTCAATTCCTGTTGCTGGAGTTCTTA 540  
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RESULT 9  
AX395213 1475 bp DNA linear PAT 18-MAY-2002  
LOCUS AX395213  
DEFINITION Sequence 1 from Patent WO216429.  
ACCESSION AX395213  
VERSION AX395213.1 GI:21066244  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,  
TITLE Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.  
JOURNAL Compositions and methods for the diagnosis and treatment of tumor  
Patent: WO 0216429-A 1 28-FEB-2002;  
Genentech, Inc. (US)

FEATURES  
source location/Qualifiers  
1..1475  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 53.7%; Score 1472; DB 6; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGCGAGAGAGACTCTGAATGAGAGGATTAGAGTGTTCAGAGAGAGA 60  
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DB 124 GGGCTCTCTTGGGCTCCAACTTGTGGGCTCACTCTAAGGCTTCTGGGGCTTTTGGGAC 183  
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QY 241 GACAGCAGTGGCTTCTCAAGGGCTCTGATGGAATGTGCCACACAGCAGCAGGCA 300  
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QY 301 CACCCAGTGTGACATCTATAGCACTTCTGGGCTTCCCGGCTGACATCCAGGCTGCCA 360  
DB 304 CACCCAGTGTGACATCTATAGCACTTCTGGGCTTCCCGGCTGACATCCAGGCTGCCA 363  
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DB 424 CATGATGACAGCTTCTTGGCCAGGATCCCGAGCCAAAGACAGATGGCGGTAGCAG 483  
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LOCUS	AX454606	1475 bp	DNA	linear	PAT 06-JUL-2002
DEFINITION	Sequence 191 from Patent WO208284.				
ACCESSION	AX454606				
VERSION	AX454606.1 GI:21713927				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCES	1 Baker,K.P., Ferrara,N., Geber,H., Gertlisen,M.B., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marseigne,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. Compositions and methods for the diagnosis and treatment of disorders involving angiotensins Patent: WO 0208284-A 191.31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Geber, Hanspeter (US) ; Gertlisen, Mary B. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marseigne, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)				
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ORIGIN					
Query Match	53.7%; Score 1472; DB 6; Length 1475;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 1472; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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DEFINITION	Sequence 491 from Patent WO0140466.		
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VERSION	AX464358.1	GI:21899195	
KEYWORDS	Homo sapiens (human)		
SOURCE			

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Denoyers, L., Filvaroff, E.,  
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Guney, A.L.,  
Sherwood, S., Smith, V., Stewart, T.A., Tamas, D., Wetanabe, C.K.,  
Wood, W.L., and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 491 07-JUN-2001;  
Genentech Inc. (US)  
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Best Local Similarity 100.0%; Pred. No. 0;  
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DB 304 CACCCAG 363  
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LOCUS AX491084  
DEFINITION Sequence 191 from Patent WO0200690.  
ACCESSION AX491084  
VERSION AX491084.1 GI:22323879  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Guney, A.L., Hillan, K.J., Mayrers, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Wetanabe, C.K., Williams, P.M., Wood, W.L.  
and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 191 03-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
Source 1. 1475  
Location/Qualifiers



/organism="Homo sapiens"  
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## ORIGIN

Query Match 53.7%; Score 1472; DB 6; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 13

AX697065

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Baton, D.L., Gao, W.Q., Pan, J., Betse, D., Pong, S., Goddard, A.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 133 28-DEC-2000;  
Genentech Inc. (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
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## ORIGIN

Query Match 53.7%; Score 1472; DB 6; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGAAGTACGCTGGCAGAGAGCTCTGAATGAGGATTTAGAGTTTCAAGAGCAGAGA 60  
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1475)
AUTHORS Clark,H.F., Gunney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hase,P.B.,
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Xie,M.H., Yansura,W.I. and Godowski,P.
Godard,A., Wood,M.D. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 1475)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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## ORIGIN

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## RESULT 15

BC014424

LOCUS

DEFINITION

Homo sapiens claudin 2, mRNA (cDNA clone MGC:20191 IMAGE:4645075),

complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1506)

1 Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Lonergan, N.A., Peters, G.J., Abramson, R.D., Muliyil, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, X., Gibbs, R.A., Viallison, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whilton, E., Kettelman, M., Madan, A., Rodriguez, Y., Bouffard, G.G., Blakeley, R.W., Madan, A., Young, A.C., Shevchenko, Y., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzinski, M.I., Skalska, U., Smallus, D.B., Schnerch, A., Schein, J.E., Jones, S.J., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16703 (2002)

12477932

2 (bases 1 to 1506)

REFERENCE

STRAUSBERG, R.

AUTHORS

TITLE

Direct Submission

## JOURNAL

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

## REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@cgsc.bc.ca](mailto:info@cgsc.bc.ca)

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabh, Parvaneh Saeedi, JR Santos, Angeliqne Scherch, Ursula Skalska, Duane Smalus, Jeff Stolt, Miranda Tsai, George Yang, Jacqui Schein, Asim Siddiqui, Rob Holt, Marco Marra.

## FEATURES

## source

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Job time : 18354 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2004, 00:32:54 ; Search time 1845 Seconds

(without alignments)  
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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 20

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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36	1472	53.7	1475	9	ADA76441	ADA76441 Human PRO
37	1472	53.7	1475	9	ADB17136	ADB17136 Human cDN
38	1472	53.7	1475	9	ADA19091	ADA19091 Human PRO
39	1472	53.7	1475	9	ADA61714	ADA61714 Homo. sap1
40	1472	53.7	1475	9	ADB19499	ADB19499 Novel hum
41	1472	53.7	1475	9	ADB28040	ADB28040 cDNA enco
42	1472	53.7	1475	9	ADA86519	ADA86519 Novel hum
43	1472	53.7	1475	9	ADA16083	ADA16083 Human PRO
44	1472	53.7	1475	9	ADA47869	ADA47869 Human PRO
45	1472	53.7	1475	9	ACH03615	ACH03615 Human sec

#### ALIGNMENTS

RESULT 1	AAAI2585	standard; cDNA, 2742 BP.
ID	AAAI2585;	
AC	AAAI2585;	
XX		
DT	25-JUL-2000	(first entry)
XX		
DE	cDNA encoding a membrane associated organizational protein (HUNCT).	
XX		
KW	Human; membrane associated organizational protein; HUNCT;	
KW	cell proliferative disorder; cancer; autoimmune disorder;	
KW	inflammatory disorder; neurological disorder; developmental disorder;	
KW	vesicle trafficking; reproductive disorder; gastrointestinal disorder;	
KW	renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;	
KW	Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;	
KW	irritable bowel syndrome; allergy; ss.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	119..811
FT		/*tag= a
FT		/product= "membrane associated organizational protein"
XX		
XX	WO200018915-A2.	
XX		
PD	06-APR-2000.	
XX		
XX		
XX	23-SEP-1999;	99WO-US022082.
XX		
XX	25-SEP-1998;	98US-0155215P.
PR	13-OCT-1998;	98US-0155215P.
PR	04-MAY-1999;	99US-0172228P.
XX		
XX	(INCY- )	INCYTE PHARM INC.
XX		
XX	Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;	
XX		
XX	WPI: 2000-293154/25.	
XX	P-PSDB; AAY84609.	
XX		
PT	Human membrane associated organizational protein and nucleic acid	
PT	sequences useful in the diagnosis, treatment and prevention of cell	





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Db 1681 ACTCTAGGGGACCTGACCTGACCTCTTGCCTAAACCAAGAGGCTATATAGCAAT 1740
Qy 1741 GGTTCCTTAGGAACAGTAAACAGTTCCTTAGAGATGACCTTGGCTGGGGATGACA 1800
Db 1741 GGTTCCTTAGGAACAGTAAACAGTTCCTTAGAGATGACCTTGGCTGGGGATGACA 1800
Qy 1801 GTGTGGAGCTGTGGGGTACTGAGGAAGACACATTCCTTGAACGATCTTAAGAGCCAG 1860
Db 1801 GTGTGGAGCTGTGGGGTACTGAGGAAGACACATTCCTTGAACGATCTTAAGAGCCAG 1860
Qy 1861 GTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Db 1861 GTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Qy 1921 AGAAACTCTTCAAGCCCTTAATGAAATACAGTCAATGAATACAGGCCCCCAGGGTCC 1980
Db 1921 AGAAACTCTTCAAGCCCTTAATGAAATACAGTCAATGAATACAGGCCCCCAGGGTCC 1980
Qy 1981 ACCCAGAGACACTACAGAGCTCTGAAAGACATAGACCAAGAGGAGCCCTTCAATTT 2040
Db 1981 ACCCAGAGACACTACAGAGCTCTGAAAGACATAGACCAAGAGGAGCCCTTCAATTT 2040
Qy 2041 CCCCACCTGTCCATCGGAGATGCTCCAGAGTGTGCTAGAGGGCATCTTAAGGGCTCCAGCA 2100
Db 2041 CCCCACCTGTCCATCGGAGATGCTCCAGAGTGTGCTAGAGGGCATCTTAAGGGCTCCAGCA 2100
Qy 2101 TGGCATATCCATGCTCCAGCGTCTGTGTCCATGATCTGATGATGCTGCTGCTCT 2160
Db 2101 TGGCATATCCATGCTCCAGCGTCTGTGTCCATGATCTGATGATGCTGCTGCTCT 2160
Qy 2161 GGGATGACAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2220
Db 2161 GGGATGACAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2220
Qy 2221 GTCCGAAATGTTCCCTTACCTCTGAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2280
Db 2221 GTCCGAAATGTTCCCTTACCTCTGAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2280
Qy 2281 TCCCTCAGCAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2340
Db 2281 TCCCTCAGCAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2340
Qy 2341 CATTCGAGAGAGAGGGCCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 CATTCGAGAGAGAGGGCCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Qy 2401 TTGCGATGTTCCAGCTGCTCTCCCAACCTGGAAGCCGCTCCCTTAGGCCAAGTCTCC 2460
Db 2401 TTGCGATGTTCCAGCTGCTCTCCCAACCTGGAAGCCGCTCCCTTAGGCCAAGTCTCC 2460
Qy 2461 TCAGAGCTGTGAGAACTTCTCAGAGGTCACTCTTCAATGAGCTTCTGATCATCTCA 2520
Db 2461 TCAGAGCTGTGAGAACTTCTCAGAGGTCACTCTTCAATGAGCTTCTGATCATCTCA 2520
Qy 2521 TCCCTCAGCAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2580
Db 2521 TCCCTCAGCAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2580
Qy 2581 CATTCAGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Db 2581 CATTCAGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Qy 2641 GTAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700
Db 2641 GTAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700
Qy 2701 GTAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2742
Db 2701 GTAAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2742

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RESULT 2

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AAFP3769
ID AAFP3769 standard; cDNA; 2863 BP.
AC AAFP3769;
DT 23-MAY-2001 (first entry)
DE Human cDNA encoding a membrane or secretory protein clone PSEC0059.
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
  rheumatoid arthritis; diabetes; ss.
OS Homo sapiens.
PN EP1067182-A2.
PD 10-JAN-2001.
PF 07-JUL-2000; 2000BP-00114090.
PR 08-JUL-1999; 994P-00194179.
PR 11-JAN-2000; 2000BP-00118775.
PR 02-MAY-2000; 2000BP-00183766.
PA (HELI-) HELIX RBS INST.
PI Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
DR WPI; 2001-093989/11.
DR P-PSDB; AAB88342.
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
  gene therapy or as candidate target molecules in drug development.
PS Claim 1; SEQ ID NO 51; 609pp + Sequence listing; English.

This invention relates to nucleic acid sequences AAFP3744 - AAFP3916
which encode human secretory or membrane proteins represented by AAB88317
- AAB88419. Included in the invention are primers AAFP3917 - AAFP4295 and
AAFP6232 - AAFP6235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polynucleotide sequences can be used in gene
therapy. The polynucleotide sequences and the proteins they encode may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used to study the expression and function of secretory
protein/membrane polypeptides and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
against them and in assays to identify modulators (agonists and
antagonists) of expression and activity. The antibodies and antagonists
may also be used as therapeutic agents to down regulate expression and
activity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in samples (e.g. by enzyme
linked immunosorbent assay (ELISA)). Examples of diseases which may be
treated include rheumatoid arthritis and diabetes

XX Sequence 2863 BP; 670 A; 794 C; 711 G; 688 T; 0 U; 0 Other;
QY
  Query Match 91.6%; Score 2513; DB 5; Length 2863;
  Best Local Similarity 99.9%; Pred. No. 0;
  Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 AGAAGTCAGCCTGAGAGAGAGCTGAAATGAGGATTAGAGGTTCAGAGAGAGAGA 60
  113 AGAAGTCAGCCTGAGAGAGAGAGCTGAAATGAGGATTAGAGGTTCAGAGAGAGAGA 172
QY 61 GCTTCAGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 173 GCTTCAGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 232

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QY	121	GGCCCTCTTGGCCCTTCCAACTTGTGGGGCTACATCCAGAGCCCTTCTGGGGCTTTTGGGAC	180
Db	233	GGCCTCTTGGCCTTCCAACTTGTGGGCTACATCCAGAGCCCTTCTGGGGCTTTTGGGAC	292
QY	181	ACTGGTTGCCATGTCTGCTCCCGAGCTGGAAAACAAGTTCTTATGTCTGGTCCAGCATTTGT	240
Db	293	ACTGGTTGCCATGTCTGCTCCCGAGCTGGAAAACAAGTTCTTATGTCTGGTCCAGCATTTGT	352
QY	241	GACAGCACTTGGCTTCTCCAAAGGGCTCTGGATGGAAATGTGCAACACAGCAACAGGCAT	300
Db	353	GACAGCACTTGGCTTCTCCAAAGGGCTCTGGATGGAAATGTGCAACACAGCAACAGGCAT	412
QY	301	CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCCCTGCGCGTGAATCACAAGCTGGCCA	360
Db	413	CACCCAGTGTGACATCTATAGCAACCTTCTGGAGCCCTGCGCGTGAATCACAAGCTGGCCA	472
QY	361	GGCCATGATGTGATGACATCATCGATGCAATCTCTCCCTGGCTTGACATTAATCTGTGTGTGG	420
Db	473	GGCCATGATGTGATGACATCATCGATGCAATCTCTCCCTGGCTTGACATTAATCTGTGTGTGG	532
QY	421	CATGGAATGCAACAGTCTTCTGCGCAAGAAATCCCGACCGAAAGACAAAGTGGGCGTTCAGG	480
Db	533	CATGGAATGCAACAGTCTTCTGCGCAAGAAATCCCGACCGAAAGACAAAGTGGGCGTTCAGG	592
QY	481	TGGAATCTTTTTCATCTCTTGGAGGCGCTCGTGGGATTTCAATTCCTGTTCCTTGAAATCTTCA	540
Db	593	TGGAATCTTTTTCATCTCTTGGAGGCGCTCGTGGGATTTCAATTCCTGTTCCTTGAAATCTTCA	652
QY	541	TGGGATCTCTAAGGGAATCTTACTACACACTGTGTGCTTGAACAGATGAAAATTTGAATTTGG	600
Db	653	TGGGATCTCTAAGGGAATCTTACTACACACTGTGTGCTTGAACAGATGAAAATTTGAATTTGG	712
QY	601	AGAGGCTCTTTTACTTTGGGGATTAATTTTCTCCCTGTTCCTCCGATAGCTGGAATGATCTCT	660
Db	713	AGAGGCTCTTTTACTTTGGGGATTAATTTTCTCCCTGTTCCTCCGATAGCTGGAATGATCTCT	772
QY	661	CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCCAACTACTACATGCTCTCAACAGCCCA	720
Db	773	CTGCTTTTCTGCTCATCTCCAGAGAAATGCTCTCCAACTACTACATGCTCTCAACAGCCCA	832
QY	721	ACCTTGTCCACAGAGAGCTCTCCAAAGCTGTGTCAACCTCCCAAAAGTCAAAGTGAAGTT	780
Db	833	ACCTTGTCCACAGAGAGCTCTCCAAAGCTGTGTCAACCTCCCAAAAGTCAAAGTGAAGTT	892
QY	781	CAATTCCTACAGCCCTGACAGGGTATGTGTGAAGAACCAAGGGGCCAGAGCTGGGGGGGTGGC	840
Db	893	CAATTCCTACAGCCCTGACAGGGTATGTGTGAAGAACCAAGGGGCCAGAGCTGGGGGGGTGGC	952
QY	841	TGGGCTGTGTAAAAACAGTGTGACAGCAACCCGAGGGGCCACAGGTGAGGGACACTACACT	900
Db	953	TGGGCTGTGTAAAAACAGTGTGACAGCAACCCGAGGGGCCACAGGTGAGGGACACTACACT	1012
QY	901	GGATCTGTCTCAGAAAGTGTCTGTGAGATTAAGCTGACTTTGGCCATTGGATTGAGCAAG	960
Db	1013	GGATCTGTCTCAGAAAGTGTCTGTGAGATTAAGCTGACTTTGGCCATTGGATTGAGCAAG	1072
QY	961	GCAGAAATGGGGGCTAGTGTAAACAGACATGACAGTGTGAATTGGCAAGAAATGCTGGCAGTGC	1020
Db	1073	GCAGAAATGGGGGCTAGTGTAAACAGACATGACAGTGTGAATTGGCAAGAAATGCTGGCAGTGC	1132
QY	1021	CAGCCTTTCTGTTTTCTCAACCTTGTCTGCCCTGCGCTTAAGTCCCAACCTCAACTT	1080
Db	1133	CAGCCTTTCTGTTTTCTCAACCTTGTCTGCCCTGCGCTTAAGTCCCAACCTCAACTT	1192
QY	1081	GAAACCCCAATTCCTTTAAGCCAGAGACTCAGAGAGATCCCTTTGGCCTCTGTGTTTACTGTGG	1140
Db	1193	GAAACCCCAATTCCTTTAAGCCAGAGACTCAGAGAGATCCCTTTGGCCTCTGTGTTTACTGTGG	1252
QY	1141	ACTGCATCCCAAAACCACTATATCATGCCCATGACTGAGCCCTGTGATCAAAAGACC	1200
Db	1253	ACTGCATCCCAAAACCACTATATCATGCCCATGACTGAGCCCTGTGATCAAAAGACC	1312

QY	1201	CTCTCTGGCGAGAGTTGGCTCTTACGCTCATGTGCGGGATGGGAGAGAAAGCAATGAGC	1260
Db	1313	TCCTCTGGCTGAGAGTTGGCTCTTAACTCATTTGCTGGGAGTGGAGAGAGACATGAGC	1372
QY	1261	TTTTGTGGGCAATGCTCTTAACTTACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC	1320
Db	1373	TTTTGTGGGCAATGCTCTTAACTTACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCC	1432
QY	1321	TGGAACCTCCATCCCACTCTTGTATTGATCTGCACAGTGTCCAGACTAATTTGTGCATGAA	1380
Db	1433	TGGAACCTCCATCCCACTCTCTGTATTGATCTGCACAGTGTCCAGACTAATTTGTGCATGAA	1492
QY	1381	CTGAATTAAGAAACCAATCCTAAGGTATCCAGGGGAAACAGAAAGCAGATCCAGGATGGGAGGA	1440
Db	1493	CTGAATTAAGAAACCAATCCTAAGGTATCCAGGGGAAACAGAAAGCAGATCCAGGATGGGAGGA	1552
QY	1441	CAGGAAGGCAAGCTTGAGACATTTTAAAAAATTAATAAATAAAAAAACCAGAACCCCATTT	1500
Db	1553	CAGGAAGGCAAGCTTGAGACATTTTAAAAAATTAATAAATAAAAAAACCAGAACCCCATTT	1612
QY	1501	TCTCAGGGCACTTTCAGAAATTCCTCATATTTGTGGCTGGGATCAAAGCTGCAAGCTTG	1560
Db	1613	TCTCAGGGCACTTTCAGAAATTCCTCATATTTGTGGGCTGGGATCAAAGCTGCAAGCTTG	1672
QY	1561	AGGAAAGCAAGGAAAGGAAAGAAAGATCTGTGTGAAAGAGCTCAGGTGGCAGCCGACCTG	1620
Db	1673	AGGAAAGCAAGGAAAGGAAAGAAAGATCTGTGTGAAAGAGCTCAGGTGGCAGCCGACCTG	1732
QY	1621	ACTCCACTGAGGAATGACCTGCTCAGAAAGCTGCGATCACAATTTGTGCTAGAGCCCTGCTC	1680
Db	1733	ACTCCACTGAGGAATGACCTGCTCAGAAAGCTGCGATCACAATTTGTGCTAGAGCCCTGCTC	1792
QY	1681	ACTCTAGGGCACTGACCTGGCCTCTTGCTTAAACCAAGGCTAATGAGCAAT	1740
Db	1793	ACTCTAGGGCACTGACCTGGCCTCTTGCTTAAACCAAGGCTAATGAGCAAT	1852
QY	1741	GGTTTCCTTAAAGAACATTAACCAAGGTTTCTTACAGGATGGCCCTTGCTGGGGGATGACA	1800
Db	1853	GGTTTCCTTAAAGAACATTAACCAAGGTTTCTTACAGGATGGCCCTTGCTGGGGGATGACA	1912
QY	1801	GTGTGGAGAGCTGTGGGGGTACTGAGAGAGACAACAATTCCTTGAACGGTCTTAAGAAAGCAG	1860
Db	1913	GTGTGGAGAGCTGTGGGGGTACTGAGAGAGACAACAATTCCTTGAACGGTCTTAAGAAAGCAG	1972
QY	1861	GTGATGTGTGTGTGGCTCCAGTGGGTGTTCTACTCTGCAAGTGAAGGAGAGCCCTT	1920
Db	1973	GTGATGTGTGTGTGGCTCCAGTGGGTGTTCTACTCTGCAAGTGAAGGAGAGCCCTT	2032
QY	1921	AGAAATCTTTCAGGCGGTATATGAAAAATCAGCTCAATATGAATCAAGGCCCCCCCAGGGTCC	1980
Db	2033	AGAAATCTTTCAGGCGGTATATGAAAAATCAGCTCAATATGAATCAAGGCCCCCCCAGGGTCC	2092
QY	1981	ACCACAGAGCACTACAGAGCCTCTGAAGACCACTACACAACAGCAGACCCTTCAGATT	2040
Db	2093	ACCACAGAGCACTACAGAGCCTCTGAAGACCACTACACAACAGCAGACCCTTCAGATT	2152
QY	2041	CCCCCACTGTCCATCGAAGATGCTCCAGATGTGCTAAGAGGCACTTAAGGGCTCCAGCA	2100
Db	2153	CCCCCACTGTCCATCGAAGATGCTCCAGATGTGCTAAGAGGCACTTAAGGGCTCCAGCA	2212
QY	2101	TGGATATTCATGCGCCACGGTGTGTGTCCATATCTGAATGATAGCTGCATCTGTGCTT	2160
Db	2213	TGGATATTCATGCGCCACGGTGTGTGTCCATATCTGAATGATAGCTGCATCTGTGCTT	2272
QY	2161	GGGATTCAGCTGAGGTGGGAGTGGAAATGTTTCCAGGAAGACATTCACCTCTAAG	2220
Db	2273	GGGATTCAGCTGAGGTGGGAGTGGAAATGTTTCCAGGAAGACATTCACCTCTAAG	2332
QY	2221	GTCCGAAATATGTTCCCTTTTACCCCTGAGATGGGAGTGAAGGGGTCTATACCAAAAGTATTT	2280
Db	2333	GTCCGAAATATGTTCCCTTTTACCCCTGAGATGGGAGTGAAGGGGTCTATACCAAAAGTATTT	2392
QY	2281	TTCCTTCACAGTTCAGGCAATGATCGGCTTCTGAAAAATTCACAGACACTTCCTTGAACCT	2340

Db	2393	TCCTTCACCACTCTAGGCATATCTGGCTTGTGAAAAATTCCAGACACCTCTCGAACT	2452
Qy	2341	CATTGTGACGAGAGAGGGCCCATCTGTTGTCTGTAACTGCGTTTCAATGTCCACCTTC	2400
Db	2453	CATTGTGACGAGAGAGGGCCCATCTGTTGTCTGTAACTGCGTTTCAATGTCCACCTTC	2512
Qy	2401	TTGGCAGTTCACAGTGTCTTCGCCAAGCTGGAAGCGGTCTCCCTTAAGCCAAATCTCC	2460
Db	2513	TTGGCAGTTCACAGTGTCTTCGCCAAGCTGGAAGCGGTCTCCCTTAAGCCAAATCTCC	2572
Qy	2461	TCAGGCTTGAGAACTTGCTCAGGGTCACTCCTTCAATGAGCGCTTCGATCACTCA	2520
Db	2573	TCAGGCTTGAGAACTTGCTCAGGGTCACTCCTTCAATGAGCGCTTCGATCACTCA	2632
Qy	2521	TCCCTCTCCATCCCTCCCTCCCTCCCAACCTCAATGTAATTAATGCTCTTGATGCTTAA	2580
Db	2633	TCCCTCTCCATCCCTCCCTCCCTCCCAACCTCAATGTAATTAATGCTCTTGATGCTTAA	2692
Qy	2581	CATTCACAATTTTGGATTGATCGTATTGTTGTGTGTGTGTCGCAATCAAGATATAT	2640
Db	2693	CATTCACAATTTTGGATTGATCGTATTGTTGTGTGTGTGTCGCAATCAAGATATAT	2752
Qy	2641	GTAACACCTTTGGGTGGGTGGGGGCAATTCCTAAGACCTCTGTGATCCCGACGATATCT	2700
Db	2753	GTAACACCTTTGGGTGGGTGGGGGCAATTCCTAAGACCTCTGTGATCCCGACGATATCT	2812
Qy	2701	GTAACAGTCCAGGAC 2717	
Db	2813	GTAACAGTCCAGGAC 2829	

### RESULT 3

ID ACC50950 standard; cDNA; 3126 BP.

AC ACC50950;

DT 12-JUN-2003 (first entry)

DE Human secreted protein BAC clone SEQ ID NO 1130.

KM Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
 KM vulnerary; antiinflammatory; nootropic; neuroprotective;

**OS Homo sapiens.**

PN WO200295010-A2.

PD 28-NOV-2002.

PF 19-MAR-2002; 2002WO-US009785.

21-MAR-2001; 2001US-0277340P.

PR 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI    Rosen CA,    Ruben SM;

DR WPI; 2003-129429/12.

PT Novel human secreted

PT disorders such as arrhythmia.

PS Disclosure; SEQ ID NO 1130; 1881pp; English

CC The present invention relates to novel human secreted proteins (ABR47633-

CC and their coding sequences are useful for the preparation of a diagnostic

or pharmaceutical composition for diagnosing or treating a cardiovascular  
 disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary  
 arteriosclerosis and myocardial ischaemia), neural disorders, immune  
 system disorders, muscular disorders, reproductive disorders,  
 gastrointestinal disorders, pulmonary disorders, renal disorders,  
 proliferative disorders and/or cancerous diseases and conditions, for  
 wound healing and epithelial cell proliferation, to treat inflammation or  
 infection, for treating thrombosis and arteriosclerosis, for treating or  
 preventing neural damage which occurs in neuronal disorders or  
 neurodegenerative conditions such as Alzheimer's disease and Parkinson's  
 disease, to enhance bone and periodontal regeneration and aid in tissue  
 transplants or bone grafts, to prevent skin aging or hair loss, to  
 stimulate growth and differentiation of haematopoietic cells and bone  
 marrow cells when used in combination with other cytokines, to maintain  
 organs before transplantation or for supporting cell culture of primary  
 tissues, to increase or decrease differentiation or proliferation of  
 embryonic stem cells, or to modulate mammalian characteristics or  
 metabolism. The present sequence was used to illustrate the invention.  
 Note: The sequence data for this patent was published in electronic  
 format and is available from WIPO at  
[ftp.wipo.int/pub/publ/published\\_pat\\_sequences](http://wipo.int/pub/publ/published_pat_sequences)

Query March	91.6%	Score 2513;	DB 8;	Length 3126;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 2713; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

**Oy**      1 AGAAGTACGCCCTGGCAGAGA GACTCTGAAA TGAGGGATTGAGGTCTTCAAGAGACAAGA 60  
**Db**      373 AGAAGTACGCCCTGGCAGAGA GACTCTGAAT TGAGGGATTGAGGTCTTCAAGAGACAAGA 432

61 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGSTCTGCCAT 120

Qy 121 GGCCCTCTCTGGCCCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 180  
|||||  
Db 493 GGCCCTCTCTGGCCCTCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 552

**Oy**            181 ACTGTTGCCATGCTGCCTCCAGCTGGAAAACAATTCTTATGTGGTGTCACGACTTGT 240  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
**D6**            553 A CTGCGTTGCCATGCTGCTCCTCCCAGCTGGAAAAACAAGTTCTTATGTGCGTGCCAGCA TGT 612  
| | | | | | | | | | | | | | | | | | | | | | | | | |

241 GACAGCAGTTGGCTTCTCCAGGGCTCTGGATGGATGGCCACACACAGCAGGCAT 300  
DB 613 GACAGCAGTTGGCTTCTCCAGGGCTCTGGATGGATGGCCACACACAGCAGGCAT 672

301 CACCCAGTGTGACATCTATAGCACCCCTTCTGGGCGCTGCCGCTGACATCCAGGCTGCCCA 360  
 673 CACCCAGTGTGACATCTATAGCACCCCTTCTGGGCGCTGCCGCTGACATCCAGGCTGCCCA 732

Oy 361 GGCCATGATGTTGCATCCAGTGCATTCCTCCCTGGCCTGCATTATCTCTGTGGGG 420  
 |||||  
 Db 733 GGCCATGATGTTGCATCCAGTGCATTCCTCCCTGGCCTGCATTATCTCTGTGGGG 792  
 |||||

421 CATGAGATGCACAGTCTTCTGCGCAGGAATCCCGACCAAGACAGAGTGGCGGTAGCAGG 480

481 TGGAGCTTTTTCATCCTGGAGGCGTCTGGGATTCATTCTGTTCCTGGATCTTCA 540

Oy 541 TGGGATCCTACGGGACTTCTACTCA CCACTGTGCTGACAGCATGAATTGAGATTGG 600  
Ox 972

601 AGAGGCTCTTACCTGGGCAATTATTCCTCCCTGTCCTCGATAGCTGGAATCATCCT 660

661 CTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAAGTACGATGCGCTTACCAAGCCCA 720



DT 03-APR-2003 (first entry)  
 XX Secreted protein gene 168 genomic fragment HTP1H83, SEQ ID NO:650.  
 XX  
 XX Human, secreted protein; digestive disorder; gastrointestinal disorder;  
 KM much; oesophagus; stomach; small intestine; large intestine; liver;  
 KM biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;  
 KM immune disorder; inflammation; infection; wound healing; drug screening;  
 KM chromosome identification; chromosome mapping; cytostatic; gene therapy;  
 KM anti-inflammatory; immunosuppressive; valnerary; chromosome Xq22.3-23;  
 KM gene; ds.  
 XX Homo sapiens.  
 XX  
 XX W020027648-A1.  
 XX  
 XX 03-OCT-2002.  
 XX  
 XX 19-MAR-2002; 2002MO-US008276.  
 XX  
 XX 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 XX WPI; 2003-022900/02.  
 XX  
 XX New human secreted proteins and nucleic acids, useful for detecting,  
 PT preventing, diagnosing, prognosticating, treating and/or ameliorating,  
 PT e.g. gastrointestinal diseases and disorders, or cancers.  
 XX  
 XX Disclosure, Page 1211-1212; 1216pp; English.  
 XX  
 XX ABZ71190-ABZ711478 represent cDNAs corresponding to 178 human secreted  
 CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.  
 CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The  
 CC invention also encompasses antibodies specific for the secreted proteins,  
 CC the use of the secreted proteins in drug screening, and recombinant  
 CC vectors and host cells comprising a nucleic acid of the invention. The  
 CC secreted proteins, nucleic acids encoding them, antibodies or antibody  
 CC fragments specific for the secreted proteins, and modulators of protein  
 CC activity are useful for diagnosing, treating, ameliorating or preventing  
 CC digestive disorders. Such conditions include disorders of the mouth,  
 CC oesophagus, stomach, small intestine, large intestine, liver, biliary  
 CC tract and pancreas, and include cancers of these organs and tissues. The  
 CC secreted proteins and their nucleic acids may also be used in the  
 CC treatment of immune disorders, inflammation, infection,  
 CC hyperproliferative disorders, and to promote wound healing. Nucleic acids  
 CC of the invention may be used for chromosome identification, chromosome  
 CC mapping, in gene therapy, for identifying individuals from minute  
 CC biological samples, as hybridisation probes, and as molecular weight  
 CC markers. The present sequence represents a human secreted protein genomic  
 CC fragment referred to in the disclosure of the invention  
 XX  
 XX Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;  
 SQ  
 Query Match 91.6%; Score 2513; DB 8; Length 3126;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 493 GGCTCTCTTGAGCTCCAACTTGAGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 552  
 QY 181 ACTGTTGCGATGCTGCTGCCAGCTGAGAAAAGAGTTCTTATGCGTCCAGCATTTGT 240  
 Db 553 ACTGTTGCGATGCTGCTGCCAGCTGAGAAAAGAGTTCTTATGCGTCCAGCATTTGT 612  
 QY 241 GACAGCATTTGCTTCCAAAGGAGCTCTGGAATGATGCCACACAGCAGAGCAT 300  
 Db 613 GACAGCATTTGCTTCCAAAGGAGCTCTGGAATGATGCCACACAGCAGAGCAT 672  
 QY 301 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGCGCGCTGACATCCAGCTCCCA 360  
 Db 673 CACCCAGTGTGACATCTATGACACCTTCTGGGCTGCGCGCTGACATCCAGCTCCCA 732  
 QY 361 GGCATGATGATGACATCCAGTGAATCTCTCCCTGGAGCTGATTAATCTGAGTGGG 420  
 Db 733 GGCATGATGATGACATCCAGTGAATCTCTCCCTGGAGCTGATTAATCTGAGTGGG 792  
 QY 421 CATGATGACAGTCTTCTGCGAGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480  
 Db 793 CATGATGACAGTCTTCTGCGAGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 852  
 QY 481 TGAAGTCTTTTATCTCTGAGGCTCTGAGATTCATCTCTGTTGCTGGAATCTTCA 540  
 Db 853 TGAAGTCTTTTATCTCTGAGGCTCTGAGATTCATCTCTGTTGCTGGAATCTTCA 912  
 QY 541 TGGAGTCTTACGAGGACTTCTACTACCACTGAGGCTGACAGATGAATTTAGATTGG 600  
 Db 913 TGGAGTCTTACGAGGACTTCTACTACCACTGAGGCTGACAGATGAATTTAGATTGG 972  
 QY 601 AGAGGCTCTTATCTTGGGCTATTTCTTCTCTGTTCTCTCTGATGATGATTCATCT 660  
 Db 973 AGAGGCTCTTATCTTGGGCTATTTCTTCTCTGTTCTCTCTGATGATGATTCATCT 1032  
 QY 661 CTGCTTTCTGCTCATTCACAGAAATGCTGCTCAATCTAGATGCTTCAAGCCCA 720  
 Db 1033 CTGCTTTCTGCTCATTCACAGAAATGCTGCTCAATCTAGATGCTTCAAGCCCA 1092  
 QY 721 ACTCTTCCACAGAGAGCTCTCAAGGCTGCTCAACCTCCCAAGTCAAGATGAGTT 780  
 Db 1093 ACTCTTCCACAGAGAGCTCTCAAGGCTGCTCAACCTCCCAAGTCAAGATGAGTT 1152  
 QY 781 CAATCTCTACAGCTCAAGGATGATGTAAGAAACAGAGGCTCAGAGCTGAGGCTGAGC 840  
 Db 1153 CAATCTCTACAGCTCAAGGATGATGTAAGAAACAGAGGCTCAGAGCTGAGGCTGAGC 1212  
 QY 841 TGGGCTCTGTAAGAAACAGTGAAGACACCCGAGGCTCAAGGATGAGGACATCACT 900  
 Db 1213 TGGGCTCTGTAAGAAACAGTGAAGACACCCGAGGCTCAAGGATGAGGACATCACT 1272  
 QY 901 GATTCGTGTAAGAGTGTCTGAGATGATGATGATGATGATGATGATGATGATGATG 960  
 Db 1273 GATTCGTGTAAGAGTGTCTGAGATGATGATGATGATGATGATGATGATGATGATG 1332  
 QY 961 GCAAAATGAGGCTGATGTAAGATGATGATGATGATGATGATGATGATGATGATG 1020  
 Db 1333 GCAAAATGAGGCTGATGTAAGATGATGATGATGATGATGATGATGATGATGATG 1392  
 QY 1021 CAGCTTTCTGTTTCTCACTTGTCTGCTCCCTGCTCCCTGATGCTCCCACTCACTT 1080  
 Db 1393 CAGCTTTCTGTTTCTCACTTGTCTGCTCCCTGCTCCCTGATGCTCCCACTCACTT 1452  
 QY 1081 GAAACCCCATTCCTTTAAGCAGAGTCAAGAGATCCCTTTGCTCTGTTTAACTGGG 1140  
 Db 1453 GAAACCCCATTCCTTTAAGCAGAGTCAAGAGATCCCTTTGCTCTGTTTAACTGGG 1512  
 QY 1141 ACTCATCCCAACCACTAATCAATCCCACTGATGACCTCTGTGATCAAAAGCC 1200  
 Db 1513 ACTCATCCCAACCACTAATCAATCCCACTGATGACCTCTGTGATCAAAAGCC 1572  
 QY 1201 TCTCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260  
 Db 1573 TCTCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1632

QY 1261 TTTTGGGGATTGCTCTTAACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1320  
 DB 1633 TTTTGGGGATTGCTCTTAACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1692  
 QY 1321 TGGAACTCTCAATCCCACTCTTTTATATGACTCCACAGTGTCCAGACTAATTTTGTGCAATGA 1380  
 DB 1693 TGGAACTCTCAATCCCACTCTTTTATATGACTCCACAGTGTCCAGACTAATTTTGTGCAATGA 1752  
 QY 1381 CTGAAATTAATTAACCATCTCAAGGTATCCAGGGAACAGAAAGCAGGATSCAGATGAGAGA 1440  
 DB 1753 CTGAAATTAATTAACCATCTCAAGGTATCCAGGGAACAGAAAGCAGGATSCAGATGAGAGA 1812  
 QY 1441 CAGAAAGCAGCCTGGGACATTTTAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500  
 DB 1813 CAGAAAGCAGCCTGGGACATTTTAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1872  
 QY 1501 TCTCAGGGCACTTCCAGAAATCTCTCAATTTTGTGGGCTGGGATCAAGCTTCAGACTTG 1560  
 DB 1873 TCTCAGGGCACTTCCAGAAATCTCTCAATTTTGTGGGCTGGGATCAAGCTTCAGACTTG 1932  
 QY 1561 AGGAAAGCAGAAAGAAAGAAAGAAAGATCTGTGGAAGCTCAGGTGGCAGCGACTCTG 1620  
 DB 1933 AGGAAAGCAGAAAGAAAGAAAGAAAGATCTGTGGAAGCTCAGGTGGCAGCGACTCTG 1992  
 QY 1621 ACTTCACTGAGAACTGCTCAGAAAGCTGCATCAAACTTTGGCTGAGCCCCCTGCTC 1680  
 DB 1993 ACTTCACTGAGAACTGCTCAGAAAGCTGCATCAAACTTTGGCTGAGCCCCCTGCTC 2052  
 QY 1681 ACTCTAGGGCACTGACCTGCTCTTGTCTTAAACCAAGGCTAAGGGCTATAGACAT 1740  
 DB 2053 ACTCTAGGGCACTGACCTGCTCTTGTCTTAAACCAAGGCTAAGGGCTATAGACAT 2112  
 QY 1741 GGTTCCTTAAGAAACAGTAAACAGTTTCTAAGGATGGCCCTTGGCTGGGGATGACA 1800  
 DB 2113 GGTTCCTTAAGAAACAGTAAACAGTTTCTAAGGATGGCCCTTGGCTGGGGATGACA 2172  
 QY 1801 GTGTGGAGCTGTGGGCTACTGAGAAAGACACATTCCTTGAACGGTCTTAAGAGCCAG 1860  
 DB 2173 GTGTGGAGCTGTGGGCTACTGAGAAAGACACATTCCTTGAACGGTCTTAAGAGCCAG 2232  
 QY 1861 GTGGATGT 1920  
 DB 2233 GTGGATGT 2292  
 QY 1921 AGAACTCTTCAAGGCTGATGAAATCAGCTCAATGAGATCAGGCCGCCGCCAGGGTCC 1980  
 DB 2293 AGAACTCTTCAAGGCTGATGAAATCAGCTCAATGAGATCAGGCCGCCGCCAGGGTCC 2352  
 QY 1981 ACCCAGAGACATCAAGAGCTCTGAAAGACCAATAGCACCAAGCCAGCCCTTCAGATT 2040  
 DB 2353 ACCCAGAGACATCAAGAGCTCTGAAAGACCAATAGCACCAAGCCAGCCCTTCAGATT 2412  
 QY 2041 CCCCCACTGTCTCATCGGAATGTCTCAGAGTGTCTGAGGGACTCTAAGGGCTCCAGCA 2100  
 DB 2413 CCCCCACTGTCTCATCGGAATGTCTCAGAGTGTCTGAGGGACTCTAAGGGCTCCAGCA 2472  
 QY 2101 TGGCATATCATGCCCCAGGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
 DB 2473 TGGCATATCATGCCCCAGGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2532  
 QY 2161 GGGATTCAGCTGAGGTGGAGTGGAGATGTTCACAGGAAGCAATTCACACTCTAAG 2220  
 DB 2533 GGGATTCAGCTGAGGTGGAGTGGAGATGTTCACAGGAAGCAATTCACACTCTAAG 2592  
 QY 2221 GTCCGAAATATGTTTCTTTTAACTCTGAGTGGAGTGAAGGGTCTATACCAAGATATTT 2280  
 DB 2593 GTCCGAAATATGTTTCTTTTAACTCTGAGTGGAGTGAAGGGTCTATACCAAGATATTT 2652  
 QY 2281 TCCTTCAACGCTTGAAGCAATGAGCTTCTGAAATTTCTCAGACACCTCTCTGAACT 2340  
 DB 2653 TCCTTCAACGCTTGAAGCAATGAGCTTCTGAAATTTCTCAGACACCTCTCTGAACT 2712

QY 2341 CATTCACAGAGAGAGGGCCCATCTGTCTCTGTAAACATGCTTTCACATGCTCACTTC 2400  
 DB 2713 CATTCACAGAGAGAGGGCCCATCTGTCTCTGTAAACATGCTTTCACATGCTCACTTC 2772  
 QY 2401 TTGCGATGTTCAGCTGTCTCTCCAACTGGAAGGCGCTCTCCCTTACCAAGTCTCC 2460  
 DB 2773 TTGCGATGTTCAGCTGTCTCTCCAACTGGAAGGCGCTCTCCCTTACCAAGTCTCC 2832  
 QY 2461 TCAGGCTTGAAGAACTTCTCAAGCTGACCTCTCTTCAATGAGCTTCTGTATCACTCA 2520  
 DB 2833 TCAGGCTTGAAGAACTTCTCAAGCTGACCTCTCTTCAATGAGCTTCTGTATCACTCA 2892  
 QY 2521 TCCCTCTCTACCCCTCTCCCTCCCAACCTCTCAATTAATTAATTAATTAATTAATTAAT 2580  
 DB 2893 TCCCTCTCTACCCCTCTCCCTCCCAACCTCTCAATTAATTAATTAATTAATTAATTAAT 2952  
 QY 2581 CATTCACAAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
 DB 2953 CATTCACAAATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3012  
 QY 2641 GTAAACCTTGTGGGTGGGGCCATATCTTAAGCTCTCTGTATCCCTCAGACTATCT 2700  
 DB 3013 GTAAACCTTGTGGGTGGGGCCATATCTTAAGCTCTCTGTATCCCTCAGACTATCT 3072  
 QY 2701 GTAAACGTGCCAGGCAC 2717  
 DB 3073 GTAAACGTGCCAGGCAC 3089

RESULT 5  
 ADB91911  
 ID ADB91911 standard; DNA; 3126 BP.  
 XX  
 AC ADB91911;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human secreted protein related DNA #SEQ ID 857.  
 XX  
 KM Secreted protein; gene therapy; antidiabetic; diabetes; human; da.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003004622-A2.  
 PD  
 XX 16-JAN-2003.  
 PF 19-MAR-2002; 2002MO-US008124.  
 XX  
 XX 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 XX  
 DR WPI, 2003-229407/22.  
 PT Nucleic acid encoding a human secreted protein is useful in diagnosing or  
 PT treating diabetes or conditions related to diabetes.  
 XX  
 XX Disclosure; SEQ ID NO 857; 1537bp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules ADB91065-  
 CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-  
 CC ADB91834. Also disclosed is a recombinant vector comprising a  
 CC polynucleotide of the invention, and a recombinant host cell comprising  
 CC the recombinant vector. The polypeptide of the invention is useful in  
 CC identifying a binding partner by contacting the polypeptide with a  
 CC binding partner, and determining whether the binding partner increases or  
 CC decreases activity of the polypeptide. The polypeptide, polynucleotide,  
 CC antibody or its fragment, agonist or antagonist are useful for preparing



CC a pharmaceutical composition for diagnosing or treating diabetes or  
CC conditions related to diabetes. The present sequence is that of the human  
CC immunoglobulin Fc portion used to generate fusion proteins, increasing  
CC the stability of the fused protein as compared to the secreted protein  
CC only. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;

Query Match 91.6%; Score 2513; DB 9; Length 3126;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 AGAAGTCAGCCTGGCAGAGAGACTCTGAATAGAGATTAGAGTGTTCAGAGCAGAGA 60
DB 373 AGAAGTCAGCCTGGCAGAGAGACTCTGAATAGAGATTAGAGTGTTCAGAGCAGAGA 432
QY 61 GCTTCAGCCTGAAGACAGAGGAGCAGCTCCCTGAAGACGCTTCTAAGAGGTCCTGCAT 120
DB 433 GCTTCAGCCTGAAGACAGAGGAGCAGCTCCCTGAAGACGCTTCTAAGAGGTCCTGCAT 492
QY 121 GGCCTCTCTGGCCTCCAACTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 180
DB 493 GGCCTCTCTGGCCTCCAACTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 552
QY 181 ACTGGTTGCAATGTGTCTCCCACTGGGAGTGAAGAAAGTTCTTATGTGGTCCAGCATTTGT 240
DB 553 ACTGGTTGCAATGTGTCTCCCACTGGGAGTGAAGAAAGTTCTTATGTGGTCCAGCATTTGT 612
QY 241 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGCAGAGCAT 300
DB 613 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTGCCACACAGCAGAGCAT 672
QY 301 CACCCAGTGTGACATCTAATAGCACCTTCTGGGGCTTCCCGCTGACATCCAGGCTGCCA 360
DB 673 CACCCAGTGTGACATCTAATAGCACCTTCTGGGGCTTCCCGCTGACATCCAGGCTGCCA 732
QY 361 GGCCTATGATGTGACATCCAGTGTGCAATCTCTCCCTGGCTGCTGATTTATCTGTGTGGG 420
DB 733 GGCCTATGATGTGACATCCAGTGTGCAATCTCTCCCTGGCTGCTGATTTATCTGTGTGGG 792
QY 421 CATGAGATGACAGTCTTCTGCCAGAGATCCCGACCAAGACAGATGAGGCTGAGG 480
DB 793 CATGAGATGACAGTCTTCTGCCAGAGATCCCGACCAAGACAGATGAGGCTGAGG 852
QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTTGGAGTTCAATCTCTGTGCTGGAATCTTCA 540
DB 853 TGAAGTCTTTTCAATCTTGAAGGCTCTTGGAGTTCAATCTCTGTGCTGGAATCTTCA 912
QY 541 TGGGATCTTACGGGACTTTTACTACACATGTGTGCTGACAGCATGAAATTTGAGATTGG 600
DB 913 TGGGATCTTACGGGACTTTTACTACACATGTGTGCTGACAGCATGAAATTTGAGATTGG 972
QY 601 AGAGGCTCTTTAATCTTGGGCAATTAATTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCT 660
DB 973 AGAGGCTCTTTAATCTTGGGCAATTAATTTCTTCCCTGTCTCCCTGATAGCTGGAATCATCT 1032
QY 661 CTGCTTTCTGTCTCATCCAGAGAAATGCTCCCACTAATCATGATCTCAAGAGCCA 720
DB 1033 CTGCTTTCTGTCTCATCCAGAGAAATGCTCCCACTAATCATGATCTCAAGAGCCA 1092
QY 721 ACTCTTTGGCAAGAGGCTCTCAAGGCTGTGCAACTTCCCAAGTCAAGAGTGAATT 780
DB 1093 ACTCTTTGGCAAGAGGCTCTCAAGGCTGTGCAACTTCCCAAGTCAAGAGTGAATT 1152
QY 781 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACAGAGGGGCGCAGAGCTGGGGGGTGGC 840
DB 1153 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACAGAGGGGCGCAGAGCTGGGGGGTGGC 1212
QY 841 TGGGTCTGTGAAGAAACAGTGAAGACACCCGAGGGGCGACAGGTGAAGGACATCACTACT 900
DB 1213 TGGGTCTGTGAAGAAACAGTGAAGACACCCGAGGGGCGACAGGTGAAGGACATCACTACT 1272
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QY 901 GATTCGTGACAGAGGCTGTGCTGAGATATGACTGACTTTGGCCATTTGATGAGCAAG 960
DB 1273 GATTCGTGACAGAGGCTGTGCTGAGATATGACTGACTTTGGCCATTTGATGAGCAAG 1332
QY 961 GCAAGAAATGGGGCTAGTGTAAACAGATGAGGTTGAATTTGCCAGAGATCTGCCATGTC 1020
DB 1333 GCAAGAAATGGGGCTAGTGTAAACAGATGAGGTTGAATTTGCCAGAGATCTGCCATGTC 1392
QY 1021 CAGCCTTTCTGTGTTTCTGACCTTGTGCTGCCCTCCCTCAAGTCCCAAGCTCAACTT 1080
DB 1393 CAGCCTTTCTGTGTTTCTGACCTTGTGCTGCCCTCCCTCAAGTCCCAAGCTCAACTT 1452
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGGATCCCTTGGCTCTGTGTTTAACTGGG 1140
DB 1453 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGGATCCCTTGGCTCTGTGTTTAACTGGG 1512
QY 1141 ACTTCATCCCAAGCCCAATCAATCAATCCCACTGACCTGCTGTGATCAAGACCC 1200
DB 1513 ACTTCATCCCAAGCCCAATCAATCAATCCCACTGACCTGCTGTGATCAAGACCC 1572
QY 1201 TCTCTGTGAGTGTGGTCTTATGCTATGCTGTGGGATGGGAGAGACAGATGGC 1260
DB 1573 TCTCTGTGAGTGTGGTCTTATGCTATGCTGTGGGATGGGAGAGACAGATGGC 1632
QY 1261 TTTTGGGGGCAATGTCTTAACCTACTTCAAGCTTCCCTCCCAAGAACTGATTTGGGCC 1320
DB 1633 TTTTGGGGGCAATGTCTTAACCTACTTCAAGCTTCCCTCCCAAGAACTGATTTGGGCC 1692
QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTTAATTTGTGATGA 1380
DB 1693 TGGAACTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTTAATTTGTGATGA 1752
QY 1381 CTGAATTAAGAACATCTTACGTTATCCAGGAAACAGAAACAGATGAGAGTGGAGGA 1440
DB 1753 CTGAATTAAGAACATCTTACGTTATCCAGGAAACAGAAACAGATGAGAGTGGAGGA 1812
QY 1441 CAGGAAAGGAGCTGGGAGCAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1500
DB 1813 CAGGAAAGGAGCTGGGAGCAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1872
QY 1501 TCTCAGGGGCACTTTCAGAAATCTCTCATATTTGTGGGCTGGGATCAAGCTGACCTTG 1560
DB 1873 TCTCAGGGGCACTTTCAGAAATCTCTCATATTTGTGGGCTGGGATCAAGCTGACCTTG 1932
QY 1561 AGGAAAGCAGAGAAAGAGAAAGATCTGTGTGAAGCTCAGGTGGCAGCGGACTCTG 1620
DB 1933 AGGAAAGCAGAGAAAGAGAAAGATCTGTGTGAAGCTCAGGTGGCAGCGGACTCTG 1992
QY 1621 ACTCCATGAGGAACTGGCTCAGAGCTGATCAAACTTTGGCTGAGAGCCCTGCTC 1680
DB 1993 ACTCCATGAGGAACTGGCTCAGAGCTGATCAAACTTTGGCTGAGAGCCCTGCTC 2052
QY 1681 ACTCTAGGGGCACTGACCTGCTCTTGTGCTTAAGCAAGGCTAAGGCTAATAGCAAT 1740
DB 2053 ACTCTAGGGGCACTGACCTGCTCTTGTGCTTAAGCAAGGCTAAGGCTAATAGCAAT 2112
QY 1741 GGTTCCTTAAGAAAGTAAACAGTTTCTTGAAGATGGCTTGGCTGGGGGATGACA 1800
DB 2113 GGTTCCTTAAGAAAGTAAACAGTTTCTTGAAGATGGCTTGGCTGGGGGATGACA 2172
QY 1801 GTGTGGAGCTGTGGGGTACTGAGAGAGACACATCTCTTGAAGGCTTAAGAAAGCCAG 1860
DB 2173 GTGTGGAGCTGTGGGGTACTGAGAGAGACACATCTCTTGAAGGCTTAAGAAAGCCAG 2232
QY 1861 GTGAGTGTGTGTGGCTTCAGTGGGTTTCTACTGTGCAAGTGAAGAGGAGCCCTCCT 1920
DB 2233 GTGAGTGTGTGTGGCTTCAGTGGGTTTCTACTGTGCAAGTGAAGAGGAGCCCTCCT 2292
QY 1921 AGAAACTCTTCAAGGCTTAATGAAATTCAGCTCAATGAGATCAAGCCCTCCAGGCTCC 1980
DB 2293 AGAAACTCTTCAAGGCTTAATGAAATTCAGCTCAATGAGATCAAGCCCTCCAGGCTCC 2352
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QY	1981	ACCCACAGAGCACTACAGAGCCTCTGAAAGACCAATAGACCAAGAGAGCCCTCTCAGATT	2040
Db	2353	ACCACAGAGCACTACAGAGCCTCTGAAAGACCAATAGACCAAGAGAGCCCTCTCAGATT	2412
QY	2041	CCCCCACTGTCCATCGGAAGATGCTCCAGAGTGCTAGAGGGCATCTAAGGGCTCCAGCA	2100
Db	2413	CCCCCACTGTCCATCGGAAGATGCTCCAGAGTGCTAGAGGGCATCTAAGGGCTCCAGCA	2472
QY	2101	TGGCATATCCATGCCCAAGGTGCTGTGTTCATGATCTGAAGTATAGCTGCACTGTGCT	2160
Db	2473	TGGCATATCCATGCCCAAGGTGCTGTGTTCATGATCTGAAGTATAGCTGCACTGTGCT	2532
QY	2161	GGGATTTGAGCGCTGAGGTGGGAGTGGGAGATGGTTCCAGGAAGACAGTTCCACCTTAAG	2220
Db	2533	GGGATTTGAGCGCTGAGGTGGGAGTGGGAGATGGTTCCAGGAAGACAGTTCCACCTTAAG	2522
QY	2221	GTCCGAAATATGTTCCCTTTACCTTGGAGTGGGAGTGAAGGGGTCAATACCAAGATATTT	2280
Db	2593	GTCCGAAATATGTTCCCTTTACCTTGGAGTGGGAGTGAAGGGGTCAATACCAAGATATTT	2652
QY	2281	TCCCTCAACAGTCTAAGGCATGACTGGCTTTCTGAAAATTTCCAGCACACTCTCGAAGCT	2340
Db	2653	TCCCTCAACAGTCTAAGGCATGACTGGCTTTCTGAAAATTTCCAGCACACTCTCGAAGCT	2712
QY	2341	CATTGTACAGCAGAGAGGGGCCCATCTGTGTCTGTAACTATGCTTTCAATATGCCACTTC	2400
Db	2713	CATTGTACAGCAGAGAGGGGCCCATCTGTGTCTGTAACTATGCTTTCAATATGCCACTTC	2722
QY	2401	TTGCCATATTCAGAGCTGCTCTCCCAACTGGAAGGCCGCTCTCCCTTAGCCAAAGTCTCC	2460
Db	2773	TTGCCATATTCAGAGCTGCTCTCCCAACTGGAAGGCCGCTCTCCCTTAGCCAAAGTCTCC	2832
QY	2461	TCAGGCTTTGAGAACTTCTCTCAGCGTCACTCTTCATTAGACCTTCTGTATCATCTCA	2520
Db	2833	TCAGGCTTTGAGAACTTCTCTCAGCGTCACTCTTCATTAGACCTTCTGTATCATCTCA	2892
QY	2521	TCCCTCTCTCAACCCCTCCCTCCCAACCCCTCAAGTAAATTAATGCTCTTGAGGCTTAA	2580
Db	2893	TCCCTCTCTCAACCCCTCCCTCCCAACCCCTCAAGTAAATTAATGCTCTTGAGGCTTAA	2952
QY	2581	CATTCACAATTTTATATGATCGTATATTGTGTGTGTGTGCCATCTCAAGATATTT	2640
Db	2953	CATTCACAATTTTATATGATCGTATATTGTGTGTGTGTGCCATCTCAAGATATTT	3012
QY	2641	GTAAACCCCTTGCGTGGGTGGGGCCATATCTAGACCTCTCTGATATCCCGAGACTATCT	2700
Db	3013	GTAAACCCCTTGCGTGGGTGGGGCCATATCTAGACCTCTCTGATATCCCGAGACTATCT	3072
QY	2701	GTAAACGTCGACGAGCAC 2717	
Db	3073	GTAAACGTCGACGAGCAC 3089	
RESULT 6			
ADCT4722			
ID	ADCT4722	standard; DNA; 3126 BP.	
AC	ADCT4722;		
XX			
DT	01-JAN-2004	(first entry)	
XX			
DE	Human secreted protein-related DNA - SEQ ID 1355.		
XX			
KW	antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;		
KW	antidiabetic; immunosuppressive; dermatological; nephrotropic;		
KW	antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;		
KW	fungicide; antiparasitic; antilariclosclerotic; vulnerary; cytostatic;		
KW	haemopoietic; haematologic; anaemia; autoimmune disorder;		
KW	rheumatoid arthritis; inflammation; Grave's disease; diabetes;		
KW	systemic lupus erythematosus; glomerulonephritis; neurodegenerative;		
KW	Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;		
KW	cancer; bacterial; viral; fungal; parasitic infection; gene therapy;		
KW	human; ds.		

XX	Homo sapiens.
OS	
XX	WO2003038063-A2.
PN	
XX	
PD	08-MAY-2003.
XX	
PE	19-MAR-2002; 2002MO-US008277.
XX	
PR	21-MAR-2001; 2001US-0277340P.
PR	19-JUL-2001; 2001US-0306171P.
PR	13-NOV-2001; 2001US-0331287P.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
P1	Rosen CA, Ruben SM;
DR	WPI; 2003-430516/40.
XX	
PT	New human secreted polypeptide for diagnosing, preventing or treating
PT	hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT	disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT	atherosclerosis).
XX	
PS	Disclosure; SEQ ID NO 1355; 2272pp; English.
XX	
CC	The invention relates to a novel human secreted polypeptide comprising a
CC	defined sequence given in the specification. The polypeptide, nucleic
CC	acid molecule, antibody, agonist or antagonist of the invention may be
CC	useful for preparing a composition for diagnosing or treating a
CC	haemopoietic or haematologic disorder such as anaemia, autoimmune
CC	disorders, systemic rheumatoid arthritis, inflammation, Grave's disease,
CC	diabetes, systemic lupus erythematosus or glomerulonephritis,
CC	neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC	diseases, wounds and hyperproliferative disorders including
CC	atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC	parasitic infections. The polypeptide may also be used during gene
CC	therapy procedures and for identifying a binding partner by contacting
CC	the polypeptide with a binding partner and determining whether the
CC	binding partner increases or decreases the activity of the polypeptide.
CC	The current sequence is that of the human secreted protein-related DNA of
CC	the invention.
CC	
SQ	Sequence 3126 BP; 739 A; 848 C; 761 G; 778 T; 0 U; 0 Other;
	Query Match 91.6%; Score 2513; DB 10; Length 3126;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1 AGAAGTCACGCTGGCAGAGAGACTCTGAATATGAGGATTAGAGGTGTTCAAGAGACAGA 60 
DB	373 AGAAGTACCGCTGGCAGAGAGACTCTGAATATGAGGATTAGAGGTGTTCAAGAGACAGA 432 
OY	61 GCTTGACCTGAAGACAAGGGAGCATGTCCTGAAGACGCTTCTACTGAGAGTCTGCAT 120 
DB	433 GCTTCAGGCTTAAGACAAGGGAGCATGCCCTGAAGACCTTCTACTGAGAGTCTGCAT 492 
OY	121 GGCGCTCTTGAGGCGTCAAACCTGTGGGCTAATCCTTAGACCTCTGGGGCTTTTGGGAC 180 
DB	493 GGCGCTCTTGAGGCGTCAAACCTGTGGGCTAATCCTTAGACCTTTTGGGGCTTTTGGGAC 552 
OY	181 ACTGTTGCCATGTGTGCTCCCAAGCTGAAAAACAAGTTCTTATGTGGTGCACGATTGT 240 
DB	553 ACTGTTGCCATGTGTGCTCCCAAGCTGAAAAACAAGTTCTTATGTGGTGCACGATTGT 612 
OY	241 GACAGCAAGTTGGCTTTCGAAGGGCTTGGATGGAATGTGCCACACACAGCACAGGAT 300 
DB	613 GACAGCAAGTTGGCTTTCGAAGGGCTTGGATGGAATGTGCCACACACAGCACAGGAT 672 
OY	301 CACCACAGTGAACATCTATAGCACCCCTTCTGGGCGCTGGCCGCTGACATCCAGGCTGCCA 360 
DB	673 CACCACAGTGAACATCTATAGCACCCCTTCTGGGCGCTGGCCGCTGACATCCAGGCTGCCA 732 

Oy	361	GGCCATGATGAGTGACATCAAGTGAATTCCTCCCTCGGCGTCGCAATTAATCTCTGAGTGAGG	420
Db	733	GGCCATGATGAGTGACATCAAGTGAATTCCTCCCTCGGCGTCGCAATTAATCTCTGAGTGAGG	792
Oy	421	CATGAGATGACACAGTCTTCTGCGCAGAAATCCCGAGCCAAAGACAGAGTGCGGTAGCAGG	480
Db	793	CATGAGATGACACAGTCTTCTGCGCAGAAATCCCGAGCCAAAGACAGAGTGCGGTAGCAGG	852
Oy	481	TGAGATCTTTTTCATCCTTGAAGGCTCTGAGGATTCATTCCTGTGCTGGAATCTTCA	540
Db	853	TGAGATCTTTTTCATCCTTGAAGGCTCTGAGGATTCATTCCTGTGCTGGAATCTTCA	912
Oy	541	TGGGATCTCTAAGGGACTTCTA CTCACCACTGCTGCTGACAGCATGAAATTTTGAGATTGG	600
Db	913	TGGGATCTCTAAGGGACTTCTA CTCACCACTGCTGCTGACAGCATGAAATTTTGAGATTGG	972
Oy	601	AGAGGCTCTTATCTTGAGGCAATTAATTTCTCCCTGTTCTCCCTGATGAGCTGAATCATCTCT	660
Db	973	AGAGGCTCTTATCTTGAGGCAATTAATTTCTCCCTGTTCTCCCTGATGAGCTGAATCATCTCT	1032
Oy	661	CTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAAGATGCTTCAACAAGCCCA	720
Db	1033	CTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACTAAGATGCTTCAACAAGCCCA	1092
Oy	721	ACCTTCTGCCACAGAGACTCTCCAGGCGCTGTCTCAACTCCCAAGTCAGAGATGAGTT	780
Db	1093	ACCTTCTGCCACAGAGACTCTCCAGGCGCTGTCTCAACTCCCAAGTCAGAGATGAGTT	1152
Oy	781	CAATTCTTACAGCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGAGGGGTGTGC	840
Db	1153	CAATTCTTACAGCTGACAGGGTATGTGTGAAGAACAGAGGGCCAGAGCTGAGGGGTGTGC	1212
Oy	841	TGGGTCTGTGAAGAAACAGTGAACAGACACCCGAGGGCCACAGGTAGGGGACCTTACCACT	900
Db	1213	TGGGTCTGTGAAGAAACAGTGAACAGACACCCGAGGGCCACAGGTAGGGGACCTTACCACT	1272
Oy	901	GGATGTGTCAAGAAAGTGTCTGTGAGATTAACATGACTTTGGCCATTGGAATTGAGCAAG	960
Db	1273	GGATGTGTCAAGAAAGTGTCTGTGAGATTAACATGACTTTGGCCATTGGAATTGAGCAAG	1332
Oy	961	GCAGAAATGAGGGGGCTAGTGTAAACAGCAGCAGGTGTAATTTGGCCAAAGATGCTCGCAATGC	1020
Db	1333	GCAGAAATGAGGGGGCTAGTGTAAACAGCAGCAGGTGTAATTTGGCCAAAGATGCTCGCAATGC	1392
Oy	1021	CAGCCTTTCGTGTTTCTCTCACTTGTGCTCTCCCTGACCCTAAGTCCCAACCTCAACTT	1080
Db	1393	CAGCCTTTCGTGTTTCTCTCACTTGTGCTCTCCCTGACCCTAAGTCCCAACCTCAACTT	1452
Oy	1081	GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCGCTCTGTGTTACGTGG	1140
Db	1453	GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCGCTCTGTGTTACGTGG	1512
Oy	1141	ACTCCATCCCAAAACCCCACTAATCACTCACTGACCTGCTGTGATCAAAAGACC	1200
Db	1513	ACTCCATCCCAAAACCCCACTAATCACTCACTGACCTGCTGTGATCAAAAGACC	1572
Oy	1201	TCTCTCTGAGAGGTGGCTCTTAAGCTCATTTGCTGAGGATGAGGAAGAGACAGTGGC	1260
Db	1573	TCTCTCTGAGAGGTGGCTCTTAAGCTCATTTGCTGAGGATGAGGAAGAGACAGTGGC	1632
Oy	1261	TTTTTGAGGCAATGCTCTAACCCTAATTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCC	1320
Db	1633	TTTTTGAGGCAATGCTCTAACCCTAATTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCC	1692
Oy	1321	TGGAACCTCCAACTCCACTTGTATATGACTCCAGATGCCAGACTAATTTGTGCATGAA	1380
Db	1693	TGGAACCTCCAACTCCACTTGTATATGACTCCAGATGCCAGACTAATTTGTGCATGAA	1752
Oy	1381	CTGAATATTAACCATCTCTACGGTATCCAGGGAACGAAAGCAGATGACAGATGAGGAGA	1440
Db	1753	CTGAATATTAACCATCTCTACGGTATCCAGGGAACGAAAGCAGATGACAGATGAGGAGA	1812
Oy	1441	CAGGAAGCAAGCTTGGGACATTTTAAAAATTAATAAAAAAATCCAGAACCATTT	1500

Db	1813	CAGGAAGGCAAGCCCTGGGACATTAAAAATATAAAAATGAAAAAATCCAGAACCATTT	1872
QY	1501	TCTCAGGGCACTTTCCAGAAATTTCTCATATTTGTGGGCTGGGATCAAGCTCGAGCTTG	1560
Db	1873	TCTCAGGGCACTTTCCAGAAATTTCTCATATTTGTGGGCTGGGATCAAGCTCGAGCTTG	1932
QY	1561	AGGAAGCAACAAGAAAGGAAAGAAAGATCTGGGTGAAAGCTCAGGTGGCAGCGGACCTCG	1620
Db	1933	AGGAAGCAACAAGAAAGGAAAGAAAGATCTGGGTGAAAGCTCAGGTGGCAGCGGACCTCG	1992
QY	1621	ACTCAGCTGAGGAATGCTGCTCAGAAAGCTGCATACAATTTTGCTGAAGCCCTGCTC	1680
Db	1993	ACTCAGCTGAGGAATGCTGCTCAGAAAGCTGCATACAATTTTGCTGAAGCCCTGCTC	2052
QY	1681	ACTCTAAGGGCACTGAAGCTGGCTCTTGCTCTAAACAACAAGGCTTAAGGCTATAGCAAT	1740
Db	2053	ACTCTAAGGGCACTGAAGCTGGCTCTTGCTCTAAACAACAAGGCTTAAGGCTATAGCAAT	2112
QY	1741	GGTTTCTCTTGAAGAACATTAACCAAGTTTCTTAGGATGAGCCCTTGCTGGGGATGACA	1800
Db	2113	GGTTTCTCTTGAAGAACATTAACCAAGTTTCTTAGGATGAGCCCTTGCTGGGGATGACA	2172
QY	1801	GTCATGGGAGCTGATGGGGATCTGAAGAAACAACAATTCCTTGAACGCTGCTTAAGAAGCAG	1860
Db	2173	GTCATGGGAGCTGATGGGGATCTGAAGAAACAACAATTCCTTGAACGCTGCTTAAGAAGCAG	2232
QY	1861	GTGATGTGTGTGTGGCTCCAGTGGGTGTTTCTACTCTGCACTGAGAGGCAAGCCCTT	1920
Db	2233	GTGATGTGTGTGTGGCTCCAGTGGGTGTTTCTACTCTGCACTGAGAGGCAAGCCCTT	2292
QY	1921	AGAAATCTTCAGGCGCTATATGAAAAATCAGTCAATATGATCAAGCCCCCGCAGGGTCC	1980
Db	2293	AGAAATCTTCAGGCGCTATATGAAAAATCAGTCAATATGATCAAGCCCCCGCAGGGTCC	2352
QY	1981	ACCCACAGAGCACTACAGAGCCTCTGAAAGACCTAGACAACAAGCGAGCCCTTCAGATT	2040
Db	2353	ACCCACAGAGCACTACAGAGCCTCTGAAAGACCTAGACAACAAGCGAGCCCTTCAGATT	2412
QY	2041	CCCCCACTGTCATTCGGAAGATGCTCCAGATGAGCTAGAGGGCATTTAAGGGCTCCAGCA	2100
Db	2413	CCCCCACTGTCATTCGGAAGATGCTCCAGATGAGCTAGAGGGCATTTAAGGGCTCCAGCA	2472
QY	2101	TGGCATATCCATGCCCCAGAGGTGCTGTGTCCATGATCTGAATGATGCTGCACTGCTCT	2160
Db	2473	TGGCATATCCATGCCCCAGAGGTGCTGTGTCCATGATCTGAATGATGCTGCACTGCTCT	2532
QY	2161	GGGATTCGACGTTGAGGTGGGAGTGTGAAGATGCTTCCAGAAAGCAGTTCACCTTAAG	2220
Db	2533	GGGATTCGACGTTGAGGTGGGAGTGTGAAGATGCTTCCAGAAAGCAGTTCACCTTAAG	2592
QY	2221	GTCCGAAAAATGTTCCCTTAAACCTGAGATGGGAATGAGGGTCAATACCAAGATATTT	2280
Db	2593	GTCCGAAAAATGTTCCCTTAAACCTGAGATGGGAATGAGGGTCAATACCAAGATATTT	2652
QY	2281	TCCCTCACACGCTAAGGATGAGTGGCTTGTGA AAAATTCAGACAACCTTCTTGAACCT	2340
Db	2653	TCCCTCACACGCTAAGGATGAGTGGCTTGTGA AAAATTCAGACAACCTTCTTGAACCT	2712
QY	2341	CATTGTACGACGAAAGGGCCCATCTGTTGTCTGTAACA TGGCTTTCACATGTCACCTTC	2400
Db	2713	CATTGTACGACGAAAGGGCCCATCTGTTGTCTGTAACA TGGCTTTCACATGTCACCTTC	2772
QY	2401	TTGCAATTTCCAGCTGCTTCCCAACTGGAAAGGCGTCTCCCTTAAGCCAAGTCTCC	2460
Db	2773	TTGCAATTTCCAGCTGCTTCCCAACTGGAAAGGCGTCTCCCTTAAGCCAAGTCTCC	2832
QY	2461	TCAGGCTTGAAGAACTTCTCAGCGTCACTCTTCATGAGCTTCTCTGATCACTCA	2520
Db	2833	TCAGGCTTGAAGAACTTCTCAGCGTCACTCTTCATGAGCTTCTCTGATCACTCA	2892
QY	2521	TCCCTCTCTAACCCCTCCCTCCCAACCTCAATGATATAATTGCTTCTGATGCTTAG	2580

[illegible]

PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108867P.  
 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2000-237871/20.  
 DR P-PSDB; AAY9378.  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX  
 PS Claim 2; Fig 77; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;  
 Query Match 53.7%; Score 1472; DB 3; Length 1475;  
 Best Local Similarity 100.0%; Fred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481. TGGAGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 540  
 DB 484 TGGAGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 543  
 QY 541 TGGAGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 600  
 DB 544 TGGAGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 603  
 QY 601 AGAGGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 660  
 DB 604 AGAGGCTTTTTCATCCTTGAGAGGCTCTGGAGATTCATTCTGTGCTCGAATCTTCA 663  
 QY 661 CTGCTTTTCTGCTATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGCCCA 720  
 DB 664 CTGCTTTTCTGCTATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGCCCA 723  
 QY 721 ACCTTTGCAAGAGAGCTCTCAAGGCTGCTCAACCTTCCAAAGTCAAGTGAATT 780  
 DB 724 ACCTTTGCAAGAGAGCTCTCAAGGCTGCTCAACCTTCCAAAGTCAAGTGAATT 783  
 QY 781 CAATTCTTACAGCTTGAAGGATTTGTGTGAAGAACCAAGGAGGCAAGCTGGGGGTGTC 840  
 DB 784 CAATTCTTACAGCTTGAAGGATTTGTGTGAAGAACCAAGGAGGCAAGCTGGGGGTGTC 843  
 QY 841 TGGGCTGTGAAGAAACAGTGAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
 DB 844 TGGGCTGTGAAGAAACAGTGAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903  
 QY 901 GATTCGTGCAAGAGGCTGCTGAAGATTAAGTGAATTTGGCATTTGATTTGAAGCAAG 960  
 DB 904 GATTCGTGCAAGAGGCTGCTGAAGATTAAGTGAATTTGGCATTTGATTTGAAGCAAG 963  
 QY 961 GCGAAGATGGGGGCTAGTGTGAAGAGTGAAGAGGATTTGAATTTGGCATTTGATTTGA 1020  
 DB 964 GCGAAGATGGGGGCTAGTGTGAAGAGTGAAGAGGATTTGAATTTGGCATTTGATTTGA 1023  
 QY 1021 CAGGCTTTCTGTTTCTGCTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 DB 1024 CAGGCTTTCTGTTTCTGCTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
 QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGATCCCTTTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAGAGATCCCTTTGCTGCTGCTGCTGCTGCTGCT 1143  
 QY 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGACTGACTGCTGCTGCTGCTGCTGCTGCT 1200  
 DB 1144 ACTTCATCCCAAAACCACTAATCAATCCCACTGACTGACTGCTGCTGCTGCTGCTGCTGCT 1203  
 QY 1201 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 DB 1204 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
 QY 1261 TTTTGTGGGATTTGCTTAACTTAATCTTCAAGCTTCCCTCAAGAACTGAATTTGGCCC 1320  
 DB 1264 TTTTGTGGGATTTGCTTAACTTAATCTTCAAGCTTCCCTCAAGAACTGAATTTGGCCC 1323  
 QY 1321 TGAACCTCATCCCACTCTTTGTTATGACTCAAGTGTCAAGATTAATTTGTCATGAA 1380  
 DB 1324 TGAACCTCATCCCACTCTTTGTTATGACTCAAGTGTCAAGATTAATTTGTCATGAA 1383  
 QY 1381 CTGAAGATTAAGCAATCTTAAGGATTCAGGAAACAGAAACAGAGATGAGAGGAGGA 1440  
 DB 1384 CTGAAGATTAAGCAATCTTAAGGATTCAGGAAACAGAAACAGAGATGAGAGGAGGA 1443  
 QY 1441 CAGGAAGCAGCTGAGCAATTTAAAAAATA 1472  
 DB 1444 CAGGAAGCAGCTGAGCAATTTAAAAAATA 1475  
 RESULT 8  
 AAF54296  
 ID AAF54296 standard; DNA; 1475 BP.



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Db 1324 TGGAACTTCATCCCACTTGTATGATCTCCAGAGTCCAGACTAATTGTGATGAA 1383
Qy 1381 CTGAAATTAACCATCTCTAGCGTATCCAGGAAACAGAAACAGATTCAGATGGAGGA 1440
Db 1384 CTGAAATTAACCATCTCTAGCGTATCCAGGAAACAGAAACAGATTCAGATGGAGGA 1443
Qy 1441 CAGGAAGCAGCGCTGGAGCATTTTAAAAATA 1472
Db 1444 CAGGAAGCAGCGCTGGAGCATTTTAAAAATA 1475

RESULT 9
AAS21489
ID AAS21489 standard; cDNA; 1475 BP.
AC AAS21489;
XX 24-OCT-2001 (first entry)
DE Human cDNA sequence encoding for PRO1356 polypeptide.
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
XX ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; factor VIIA; gene therapy; ss.
XX Homo sapiens.
XX MO20014046-A2.
XX 07-JUN-2001.
XX 01-DEC-2000; 2000MO-US032678.
XX
XX 01-DEC-1999; 99MO-US028301.
XX 01-DEC-1999; 99MO-US028634.
XX 02-DEC-1999; 99MO-US028551.
XX 02-DEC-1999; 99MO-US028564.
XX 02-DEC-1999; 99MO-US028565.
XX 09-DEC-1999; 99US-0170262P.
XX 16-DEC-1999; 99MO-US030095.
XX 20-DEC-1999; 99MO-US030911.
XX 20-DEC-1999; 99MO-US030999.
XX 30-DEC-1999; 99MO-US031243.
XX 30-DEC-1999; 99MO-US031274.
XX 05-JAN-2000; 2000MO-US000219.
XX 06-JAN-2000; 2000MO-US000277.
XX 06-JAN-2000; 2000MO-US000376.
XX 11-FEB-2000; 2000MO-US003565.
XX 18-FEB-2000; 2000MO-US004341.
XX 18-FEB-2000; 2000MO-US004342.
XX 22-FEB-2000; 2000MO-US004414.
XX 24-FEB-2000; 2000MO-US004914.
XX 24-FEB-2000; 2000MO-US005004.
XX 01-MAR-2000; 2000MO-US005601.
XX 02-MAR-2000; 2000MO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 10-MAR-2000; 2000MO-US006319.
XX 15-MAR-2000; 2000MO-US006884.
XX 20-MAR-2000; 2000MO-US007377.
XX 21-MAR-2000; 2000MO-US007532.
XX 30-MAR-2000; 2000MO-US008439.
XX 17-MAY-2000; 2000MO-US013705.
XX 22-MAY-2000; 2000MO-US014042.
XX 30-MAY-2000; 2000MO-US014941.
XX 02-JUN-2000; 2000MO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000MO-US020710.
XX 11-AUG-2000; 2000MO-US022031.
XX 23-AUG-2000; 2000MO-US023522.
XX 24-AUG-2000; 2000MO-US023328.
XX 08-NOV-2000; 2000MO-US030952.
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PR 10-NOV-2000; 2000MO-US030873.
XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
XX Gerltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-408281/43.
XX DR P-PSDB; AAU12417.
XX
XX isolated , secretory and transmembrane PRO polypeptide used to detect
XX other PRO polypeptides, link bioactive molecules to cells expressing PRO
XX polypeptides, and detect the presence of mammalian tumors e.g. lung,
XX breast, prostate, cervical.
XX
XX Claim 3; Fig 491; 813pp; English.
XX
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
XX polypeptides. The PRO polypeptides are useful to detect other PRO
XX polypeptides, to link bioactive molecules to cells expressing PRO
XX polypeptides, to modulate biological activities of cells expressing PRO
XX polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample. Some
XX of the 275 sequences are also useful to stimulate the release of tumour
XX necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
XX differentiation of chondrocytes, the proliferation or gene expression in
XX pericyte cells, the release of proteoglycans from cartilage, the
XX proliferation of inner ear utricular supporting cells or of T-
XX lymphocytes, the release of a cytokine from peripheral blood monocytes
XX (PBMCs), or the proliferation of endothelial cells. Some of the PRO
XX polypeptides may modulate glucose or free fatty acid uptake by skeletal
XX muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
XX VIIA. The PRO polypeptides can be used in assays to identify molecules
XX involved in binding interactions. The polynucleotides encoding PRO
XX polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy
XX
XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;
XX
XX Query Match 53.7%; Score 1472; DB 4; Length 1475;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGATTGAGGTCTTCAAGAGCAAGA 60
Db 4 AGAAGTCAGCCTGGCAGAGAGACTCTGAATGAGGATTGAGGTCTTCAAGAGCAAGA 63
Qy 61 GCTTCAGCCTGAAGAGCAAGGAGAGCCTGGAAGAGCCTTCACTGAGAGGTCTGCAAT 120
Db 64 GCTTCAGCCTGAAGAGCAAGGAGAGCCTGGAAGAGCCTTCACTGAGAGGTCTGCAAT 123
Qy 121 GGCCTCTCTGGCCTCCCAACTTGTGGGCTACATCTTAGGCTTCTGGGGCTTTTGGCAC 180
Db 124 GGCCTCTCTGGCCTCCCAACTTGTGGGCTACATCTTAGGCTTCTGGGGCTTTTGGCAC 183
Qy 181 ACTGTTGCCATGCTGCTCCCAAGGCTCTGATGGAATGAGGCAACAGACAGCAGCAT 240
Db 184 ACTGTTGCCATGCTGCTCCCAAGGCTCTGATGGAATGAGGCAACAGACAGCAGCAT 243
Qy 241 GACAGCAGTTGGCTTCTCCAAAGGCTCTGATGGAATGAGGCAACAGACAGCAGCAT 300
Db 244 GACAGCAGTTGGCTTCTCCAAAGGCTCTGATGGAATGAGGCAACAGACAGCAGCAT 303
Qy 301 CACCAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATTCAGAGGTGCGCA 360
Db 304 CACCAGTGTGACATCTATAGCAACCTTCTGGGCTGCGCGTGAATTCAGAGGTGCGCA 363
Qy 361 GGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 364 GGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
```



QY 421 CATGATGTCAGAGCTCTTCTGCGAGGATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480  
 DB 424 CATGAGATGTCAGAGCTCTTCTGCGAGGATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483  
 QY 481 TGAAGCTTTTATCTCTGAGGCGCTCTGAGGATTCATTCTGTTGCTGGAATCTTCA 540  
 DB 484 TGAAGCTTTTATCTCTGAGGCGCTCTGAGGATTCATTCTGTTGCTGGAATCTTCA 543  
 QY 541 TGGGATCTTACGAGGACTTCTACTCACTGTGCTGAGAGCATGAAATTTGAGATTTG 600  
 DB 544 TGGGATCTTACGAGGACTTCTACTCACTGTGCTGAGAGCATGAAATTTGAGATTTG 603  
 QY 601 AGAGGCTCTTACTTGGGCAATATTTTCTGTTCTGCTGATGAGTGAATCATCTT 660  
 DB 604 AGAGGCTCTTACTTGGGCAATATTTTCTGTTCTGCTGATGAGTGAATCATCTT 663  
 QY 661 CTGCTTTCTGCTGATCTCCAGAGAAATGCTCTCACTAGAGATGCTTACCAAGCCCA 720  
 DB 664 CTGCTTTCTGCTGATCTCCAGAGAAATGCTCTCACTAGAGATGCTTACCAAGCCCA 723  
 QY 721 ACCTTTGCGACAGAGGACTCTCCAGGCGTGTCAACTCCCAAGTCAAGAGTAGTT 780  
 DB 724 ACCTTTGCGACAGAGGACTCTCCAGGCGTGTCAACTCCCAAGTCAAGAGTAGTT 783  
 QY 781 CAATTCCTACAGCCTGACAGGGATATGTGTGAAGAACAGGGGCCAGAGCTGGGGGGTGGC 840  
 DB 784 CAATTCCTACAGCCTGACAGGGATATGTGTGAAGAACAGGGGCCAGAGCTGGGGGGTGGC 843  
 QY 841 TGGGCTGTGAAACAGTGGAGCAGCAGCCGAGGGGCGACAGGATGAGGGGACATCACT 900  
 DB 844 TGGGCTGTGAAACAGTGGAGCAGCAGCCGAGGGGCGACAGGATGAGGGGACATCACT 903  
 QY 901 GGATCTGTGAGAGGTGTCTGTGAGATAGACTGATCTTTGGCATTTGATGAGCAAG 960  
 DB 904 GGATCTGTGAGAGGTGTCTGTGAGATAGACTGATCTTTGGCATTTGATGAGCAAG 963  
 QY 961 GCGAAATGGGGGCTGATGTAACAGCATGCAAGTGAATTTGCCAGAGATGCTGCCATGC 1020  
 DB 964 GCGAAATGGGGGCTGATGTAACAGCATGCAAGTGAATTTGCCAGAGATGCTGCCATGC 1023  
 QY 1021 CAGGCTTTCTGTTCTCTCACTTGTGCTGCTCCCTGCGCTTAAGTCCCAAGCCGCACTT 1080  
 DB 1024 CAGGCTTTCTGTTCTCTCACTTGTGCTGCTCCCTGCGCTTAAGTCCCAAGCCGCACTT 1083  
 QY 1081 GAAACCCCATTCCTTAAAGCAGGACTCAGAGGATCCCTTTGCGCTTGTAACTGTGG 1140  
 DB 1084 GAAACCCCATTCCTTAAAGCAGGACTCAGAGGATCCCTTTGCGCTTGTAACTGTGG 1143  
 QY 1141 ACTTCATCCCAAAACCACTAATCACTCCCATGACTGACCTCTGTGATCAAAAGACC 1200  
 DB 1144 ACTTCATCCCAAAACCACTAATCACTCCCATGACTGACCTCTGTGATCAAAAGACC 1203  
 QY 1201 TCTCTGCGTGAAGTGTGGCTTAACTCACTGCTGAGGATGAGGAAAGAGAGTGGC 1260  
 DB 1204 TCTCTGCGTGAAGTGTGGCTTAACTCACTGCTGAGGATGAGGAAAGAGAGTGGC 1263  
 QY 1261 TTTTGTGGGATGTCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATGGCCC 1320  
 DB 1264 TTTTGTGGGATGTCTTAACCTACTCTCAAGCTTCCCTCAAAAGAACTGATGGCCC 1323  
 QY 1321 TGAACCTCATCCACTCTTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1380  
 DB 1324 TGAACCTCATCCACTCTTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1383  
 QY 1381 CTGAATTAACAATCTCTAGGATCAAGGAAACAGAAACAGAGATGCAAGATGGAGGA 1440  
 DB 1384 CTGAATTAACAATCTCTAGGATCAAGGAAACAGAAACAGAGATGCAAGATGGAGGA 1443  
 QY 1441 CAGGAAGCAGCCTGGGACATTTTAAAAAATA 1472  
 DB 1444 CAGGAAGCAGCCTGGGACATTTTAAAAAATA 1475

RESULT 10  
 AAS15360  
 ID AAS15360 standard; cDNA; 1475 BP.  
 XX  
 AC AAS15360;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO1356 polypeptide.  
 XX  
 KW Human; PRO1356; clone DNA64886-1601; immune-related disorder; inflammatory disorder; infectious disorder; immunodeficiency disorder; autoimmune disorder; renal disease; demyelinating disease; skin disease; KM neoplasia; transplantation associated disease; gene therapy; KM immunosuppressive; anti-inflammatory; antidiabetic; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifier  
 FT CDS 122..814  
 FT /tag= a  
 FT /product= "PRO1356 polypeptide"  
 FT sig\_peptide 122..193  
 FT /tag= b  
 FT mat\_peptide 194..811  
 FT /tag= c  
 XX  
 PN MO20016740-A2.  
 PD 13-SEP-2001.  
 XX  
 PE 01-MAR-2001; 2001MO-US006666.  
 XX  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 21-MAR-2000; 2000US-0191015P.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 01-DEC-2000; 2000MO-US032678.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Epton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL; Puma D, Watanabe CK, Wood WI, Zhang Z;  
 PT P-PSDB; AAU09178.  
 XX  
 PT Nucleic acids encoding PRO polypeptides, useful for detecting and treating immune related diseases and disorders in mammals including autoimmune diseases, inflammatory diseases and asthma.  
 XX  
 PS Claim 2; Fig 1; 122pp; English.  
 XX  
 CC The present invention relates to the isolation of 9 novel human PRO polypeptides (AAU09178-AAU09186) and the cDNA sequences encoding them.  
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444, PRO3151, PRO4322, PRO3964, PRO10008 and PRO19598. The cDNA sequences encoding these PRO polypeptides have been designated as clones DNA64886-1601, DNA64803-1553, DNA64318-2520, DNA87997, DNA89273, DNA92223-2567, DNA96973, DNA101921 and DNA145867 respectively. Compositions (e.g. vaccines) containing PRO polypeptides and methods of using these compositions are useful in the treatment and diagnosis of immune-related disorders. Such disorders include immune-mediated inflammatory disorders (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g. diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or central nervous system (e.g. Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact dermatitis), neoplasias and transplantation associated diseases. The polynucleotide sequences of the invention may be used in gene therapy.  
 CC AAS15360-AAS15368 represent cDNA sequences encoding for the novel human



CC PRO polypeptides of the invention  
 XX Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;  
 SQ Query Match 53.7%; Score 1472; DB 4; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGGCTGGCAGAGAGACTCTGAATGAGGGATTAGAGTGTTCAGAGAGAGA 60  
 DB 4 AGAAGTCAGGCTGGCAGAGAGACTCTGAATGAGGGATTAGAGTGTTCAGAGAGAGA 63  
 QY 61 GCTTCAGCTGGAAGACAGAGGAGCAGTCCCTGAAGAGCTTCTACTGAGAGTCTGCAT 120  
 DB 64 GCTTCAGCTGGAAGACAGAGGAGCAGTCCCTGAAGAGCTTCTACTGAGAGTCTGCAT 123  
 QY 121 GGCCTCTCTTGGCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 180  
 DB 124 GGCCTCTCTTGGCCTCCCACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGAC 183  
 QY 181 ACTGGTTCAGATGCTGCTCCCGAGCTGGAAAAAGAGTCTTATGTGGTCCAGCATTT 240  
 DB 184 ACTGGTTCAGATGCTGCTCCCGAGCTGGAAAAAGAGTCTTATGTGGTCCAGCATTT 243  
 QY 241 GACAGCAGTTGGCTTCTCAAGGGCTCTGGATGAAATGTGCCACACAGCAGCAGGAT 300  
 DB 244 GACAGCAGTTGGCTTCTCAAGGGCTCTGGATGAAATGTGCCACACAGCAGCAGGAT 303  
 QY 301 CACCCAGTGTGACATCTATAGCACCTTCTGGGCTGGCCGCTGACATCCAGGCTGCCA 360  
 DB 304 CACCCAGTGTGACATCTATAGCACCTTCTGGGCTGGCCGCTGACATCCAGGCTGCCA 363  
 QY 361 GGCAGATGATGTGACATCCAGTGAATCTCTCCCTGGCTGCAATATCTGTGGTGG 420  
 DB 364 GGCAGATGATGTGACATCCAGTGAATCTCTCCCTGGCTGCAATATCTGTGGTGG 423  
 QY 421 CATGAGATGACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGATGGCGGTAGCAG 480  
 DB 424 CATGAGATGACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGATGGCGGTAGCAG 483  
 QY 481 TGGAGTCTTTTTCATCTTGAAGGCTCTCGGAGTTGATCTCTGTGCTCGAATCTTCA 540  
 DB 484 TGGAGTCTTTTTCATCTTGAAGGCTCTCGGAGTTGATCTCTGTGCTCGAATCTTCA 543  
 QY 541 TGGGATCTTACGGGACTTCTACTACACATCTGTGCTGACAGCAGTGAATTTGAGATT 600  
 DB 544 TGGGATCTTACGGGACTTCTACTACACATCTGTGCTGACAGCAGTGAATTTGAGATT 603  
 QY 601 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATCT 660  
 DB 604 AGAGGCTCTTACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATCT 663  
 QY 661 CTGCTTTCTGTGCTCATCCAGAGAAATCGTCCCACTACTACGATCCCAAGGCCA 720  
 DB 664 CTGCTTTCTGTGCTCATCCAGAGAAATCGTCCCACTACTACGATCCCAAGGCCA 723  
 QY 721 ACCTCTTCCACAGAGAGCTCTCAAGGCTGTGCAACCTCCCAAGTCAAGAGTGATT 780  
 DB 724 ACCTCTTCCACAGAGAGCTCTCAAGGCTGTGCAACCTCCCAAGTCAAGAGTGATT 783  
 QY 781 CAATTCCTACAGCTGACAGGATATGTGTGAAGAACAGGGGCGCAGAGCTGGGGGGTGGC 840  
 DB 784 CAATTCCTACAGCTGACAGGATATGTGTGAAGAACAGGGGCGCAGAGCTGGGGGGTGGC 843  
 QY 841 TGGGCTGTGAAAAACAGTGAAGACACCCCGAGGGCCACAGTGAAGGACACTACCACT 900  
 DB 844 TGGGCTGTGAAAAACAGTGAAGACACCCCGAGGGCCACAGTGAAGGACACTACCACT 903  
 QY 901 GGAATGCTGTCAAGAGGCTGTGCTGAGAGATAGACTGACTTTGGCCATTGGATTCAGCA 960  
 DB 904 GGAATGCTGTCAAGAGGCTGTGCTGAGAGATAGACTGACTTTGGCCATTGGATTCAGCA 963  
 QY 961 GCAGAAATGGGGCTAGTGTACAGCATGACAGTTGAATTGCCAAGATGCTGCCCATGC 1020

DB 964 GCAGAAATGGGGCTAGTGTACAGCATGACAGTTGAATTTGCCAAGATGCTGCCATGC 1023  
 QY 1021 CAGCCTTCTGTGTTTCTACACCTTGTGCTCCCTGAGTGTGCTCAACCTCAACTT 1080  
 DB 1024 CAGCCTTCTGTGTTTCTACACCTTGTGCTCCCTGAGTGTGCTCAACCTCAACTT 1083  
 QY 1081 GAAACCCCATTCCTTAAAGCAGAGTCTCAGAGATCCCTTGGCTCTGATTACCTGGG 1140  
 DB 1084 GAAACCCCATTCCTTAAAGCAGAGTCTCAGAGATCCCTTGGCTCTGATTACCTGGG 1143  
 QY 1141 ACTCCATCCCAACCCCACTATCAATCCCACTGACTGACCTCTGTGTATCAAAAGCC 1200  
 DB 1144 ACTCCATCCCAACCCCACTATCAATCCCACTGACTGACCTCTGTGTATCAAAAGCC 1203  
 QY 1201 TCTCTGTGCTGAGTGTGCTCTTACCTGATGCTGCTGGGAGTGGGAGAGAGCAGTGGC 1260  
 DB 1204 TCTCTGTGCTGAGTGTGCTCTTACCTGATGCTGCTGGGAGTGGGAGAGAGCAGTGGC 1263  
 QY 1261 TTTTGTGGCATGTCTTAACTTCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC 1320  
 DB 1264 TTTTGTGGCATGTCTTAACTTCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC 1323  
 QY 1321 TGGAACTTCATCCCACTCTTGTATGACTCCAGGTTCAGACTTAATTTGTGATGAA 1380  
 DB 1324 TGGAACTTCATCCCACTCTTGTATGACTCCAGGTTCAGACTTAATTTGTGATGAA 1383  
 QY 1381 CTGAAATTAACCATCTTACGATATCCAGGAAACAGAAAGCAGAGTGGAGGA 1440  
 DB 1384 CTGAAATTAACCATCTTACGATATCCAGGAAACAGAAAGCAGAGTGGAGGA 1443  
 QY 1441 CAGAAAGCAGCTGGGACATTTAAAAATA 1472  
 DB 1444 CAGAAAGCAGCTGGGACATTTAAAAATA 1475

RESULT 11  
 AAF92097  
 ID AAF92097 standard; cDNA; 1475 BP.  
 XX AAF92097;  
 AC AAF92097;  
 XX 15-MAY-2001 (first entry)  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human PRO1356 cDNA.  
 XX Human; PRO protein; mapping; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX  
 PN W0200116318-A2.  
 XX  
 XX 08-MAR-2001.  
 PD 08-MAR-2001.  
 PF 24-AUG-2000; 2000MO-US023328.  
 XX  
 PR 01-SEP-1999; 99MO-US020111.  
 PR 15-SEP-1999; 99MO-US021090.  
 PR 07-DEC-1999; 99US-0169495P.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 11-JAN-2000; 2000US-0175481P.  
 PR 18-FEB-2000; 2000MO-US004341.  
 PR 18-FEB-2000; 2000MO-US004342.  
 PR 22-FEB-2000; 2000MO-US004414.  
 PR 01-MAR-2000; 2000MO-US005601.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 30-MAR-2000; 2000MO-US009439.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 05-JUN-2000; 2000US-0209832P.  
 XX  
 PA (GETH ) GENENTECH INC.



PN US2002119130-A1.  
 XX 29-AUG-2002.  
 XX 06-DEC-2001; 2001US-00006867.  
 XX 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 22-APR-1998; 98US-0082797P.  
 PR 29-APR-1998; 98US-0083495P.  
 PR 15-MAY-1998; 98US-0085579P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088740P.  
 PR 10-JUN-1998; 98US-0088811P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 19-JUN-1998; 98US-0089653P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 25-JUN-1998; 98US-0090688P.  
 PR 25-JUN-1998; 98US-0090696P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 10-SEP-1998; 98US-00989741P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 10-SEP-1998; 98US-0099815P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 16-SEP-1998; 98US-0100663P.  
 PR 17-SEP-1998; 98US-0100683P.  
 PR 17-SEP-1998; 98US-0100684P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 22-SEP-1998; 98US-0101279P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 30-SEP-1998; 98US-0101916P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 08-MAR-1999; 99US-00505028.  
 PR 14-MAY-1999; 99US-005010733.  
 PR 02-JUN-1999; 99US-005012252.  
 PR 01-SEP-1999; 99US-005020111.  
 PR 15-SEP-1999; 99US-005021090.  
 PR 15-SEP-1999; 99US-005021194.  
 PR 22-DEC-1999; 99US-005030720.  
 PR 18-FEB-2000; 2000US-0004341.  
 PR 18-FEB-2000; 2000US-0004342.  
 PR 22-FEB-2000; 2000US-0004414.  
 PR 01-MAR-2000; 2000US-0005601.  
 PR 30-MAR-2000; 2000US-0008439.  
 PR 22-MAY-2000; 2000US-0014042.  
 PR 02-JUN-2000; 2000US-0015264.  
 PR 23-AUG-2000; 2000US-0023522.  
 PR 24-AUG-2000; 2000US-0023328.

PR 10-NOV-2000; 2000US-0030873.  
 PR 01-DEC-2000; 2000US-0032378.  
 PR 20-DEC-2000; 2000US-0034956.  
 PR 28-FEB-2001; 2001US-0006520.  
 PR 01-MAR-2001; 2001US-0006666.  
 PR 30-MAY-2001; 2001US-0017443.  
 PR 01-JUN-2001; 2001US-0017800.  
 PR 20-JUN-2001; 2001US-0019692.  
 PR 29-JUN-2001; 2001US-0021066.  
 PR 09-JUL-2001; 2001US-0021735.  
 XX (SETH) GENENTECH INC.  
 XX  
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI; 2002-731348/79.  
 DR P-PSDB; ABG95890.  
 XX  
 XX New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating sports-related  
 PT joint problems, osteoarthritis or rheumatoid arthritis.  
 XX  
 PS Claim 2; Fig 79; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing as  
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an  
 CC extracellular domain of the proteins with their associated signal peptide  
 CC or lacking its associated signal peptide. Also included are the nucleic  
 CC acids encoding the proteins, vectors, host cells, fusion proteins and  
 CC antibodies which specifically bind to the proteins. The proteins are  
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
 CC suspected of containing an A, B, C or D polypeptide, by contacting the  
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide  
 CC conjugate in the sample, where the formation of the conjugate is  
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H,  
 CC or I polypeptide is labeled with a detectable label or is attached to a  
 CC solid support. The proteins are useful for linking a bioactive molecule  
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
 CC or I, or antibodies against them are useful for modulating a biological  
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
 CC identifying agonists or antagonists, for the preparation of a medicament  
 CC useful in the treatment of a condition which is responsive to the  
 CC proteins, as molecular weight markers for protein electrophoresis  
 CC purposes, and as therapeutic agents for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis. Nucleic acids encoding the proteins are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
 CC generate transgenic or knockout animals which are useful in the  
 CC development and screening of therapeutic useful reagents, for chromosome  
 CC identification, and in gene therapy. The antibody is useful as a  
 CC therapeutic agent, in a diagnostic assay and for affinity purification of  
 CC the protein from recombinant cell culture natural sources. The present  
 CC sequence encodes a novel secreted or transmembrane protein of the  
 CC invention

XX  
 SQ Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;  
 Query Match 53.7%; Score 1472; DB 6; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAAGCTGGCAGAGAGACTCTGAATGAGGATTAAGGTCTTCAAGAGCAGA 60  
Db 4 AGAAGTCAAGCTGGCAGAGAGACTCTGAATGAGGATTAAGGTCTTCAAGAGCAGA 63  
QY 61 GCTTCAGCTGGAAGCAAGGAGAGAGTCCCTGAAGAGCTCTCACTGAGAGGTGCAAT 120  
Db 64 GCTTCAGCTGGAAGCAAGGAGAGAGTCCCTGAAGAGAGCTCTCTAAGAGGTCTGCAAT 123  
QY 121 GGCCTCTCTTGAGCTTCCAACTTGTGGCTCAATCTAGGCTTGTGGGCTTTTGGCAC 180  
Db 124 GGCCTCTCTTGAGCTTCCAACTTGTGGCTCAATCTAGGCTTGTGGGCTTTTGGCAC 183  
QY 181 ACTGTTGCTCATGCTGCTCCCACTGGAAGAAAGAGTTCTTAATGTGGTGGCACTATGT 240  
Db 184 ACTGTTGCTCATGCTGCTCCCACTGGAAGAAAGAGTTCTTAATGTGGTGGCACTATGT 243  
QY 241 GACAGAGTGGCTTCTTCCAAAGGGCTCTGGAATGGAATGTGSCACACACAGCAGGCAAT 300  
Db 244 GACAGAGTGGCTTCTTCCAAAGGGCTCTGGAATGGAATGTGSCACACACAGCAGGCAAT 303  
QY 301 CACCCAGTGTGACATCTTAAGCACCCTTGTGGGCTGCGCTGACATCCAGGCTGCCA 360  
Db 304 CACCCAGTGTGACATCTTAAGCACCCTTGTGGGCTGCGCTGACATCCAGGCTGCCA 363  
QY 361 GGCCTATATGTGACATCTCAAGTCAATCTCTCCCTGGCTGCAATATCTGTGTGG 420  
Db 364 GGCCTATATGTGACATCTCAAGTCAATCTCTCCCTGGCTGCAATATCTGTGTGG 423  
QY 421 CATGAGATGACAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGATGAGG 480  
Db 424 CATGAGATGACAGTCTTCTGCGCAGGAATCCCGAGCCAAAGACAGATGGCGGATGAGG 483  
QY 481 TGAAGTCTTTTCACTCTTGAAGGCTCTGGAATTCATCTGTGCTGGAATCTTCA 540  
Db 484 TGAAGTCTTTTCACTCTTGAAGGCTCTGGAATTCATCTGTGCTGGAATCTTCA 543  
QY 541 TGGGATCTTCAAGGACCTTCACTCAACATCTGTGCTGCAAGCATGAAATTTGAGATTG 600  
Db 544 TGGGATCTTCAAGGACCTTCACTCAACATCTGTGCTGCAAGCATGAAATTTGAGATTG 603  
QY 601 AGAGGCTCTTCACTTGGGCAATTAATTCCTGCTGCTCCCTGATGATGATGATGATGAT 660  
Db 604 AGAGGCTCTTCACTTGGGCAATTAATTCCTGCTGCTCCCTGATGATGATGATGATGAT 663  
QY 661 CTGCTTCTCTGCTCATCCAGAGAAATCGTCCCACTACATGATGCTTCAAGGCCA 720  
Db 664 CTGCTTCTCTGCTCATCCAGAGAAATCGTCCCACTACATGATGCTTCAAGGCCA 723  
QY 721 ACCTCTTGCACAGAGGCTCTCAAGGCTGTGCAACCTGCCAAATCAAGATGATT 780  
Db 724 ACCTCTTGCACAGAGGCTCTCAAGGCTGTGCAACCTGCCAAATCAAGATGATT 783  
QY 781 CAATTCCTACAGGCTGACAGGCTATGATGAAGAACAGAGGCGCAGAGCTGGGGGGTGGC 840  
Db 784 CAATTCCTACAGGCTGACAGGCTATGATGAAGAACAGAGGCGCAGAGCTGGGGGGTGGC 843  
QY 841 TGGGCTCTGTAAGAAACAGTGAACAGCACCAGAGGCGCAGAGTGAAGGCACTACCACT 900  
Db 844 TGGGCTCTGTAAGAAACAGTGAACAGCACCAGAGGCGCAGAGTGAAGGCACTACCACT 903  
QY 901 GGAATCGTGTCAAGAGGCTGTGCTGAGATTAAGTCACTTTGGCATTGATGAAG 960  
Db 904 GGAATCGTGTCAAGAGGCTGTGCTGAGATTAAGTCACTTTGGCATTGATGAAG 963  
QY 961 GCAAGAAATGGGGGCTAGTGTAAAGCATGAGATGAAATGGCAAGGATGCTGGCAATGC 1020  
Db 964 GCAAGAAATGGGGGCTAGTGTAAAGCATGAGATGAAATGGCAAGGATGCTGGCAATGC 1023  
QY 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCACTT 1080  
Db 1024 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTGTGCTGTGATTAAGCTGGG 1140

Db 1084 GAAACCCCATTTCCCTTAAGCAGAGACTCAAGAGATCCCTTGTGCTGTGATTAAGCTGGG 1143  
QY 1141 ACTTCATCCCCAAACCACTAATCAATCCCACTGACCTGCTGTGATCAAGACCC 1200  
Db 1144 ACTTCATCCCCAAACCACTAATCAATCCCACTGACCTGCTGTGATCAAGACCC 1203  
QY 1201 TCTCTGTGCTGAGTGGTGTCTTAAGCTCATGCTGGGATGGAAGAGAGCAATGTC 1260  
Db 1204 TCTCTGTGCTGAGTGGTGTCTTAAGCTCATGCTGGGATGGAAGAGAGCAATGTC 1263  
QY 1261 TTTTGGGCAATGCTCTAAGCTTCAAGCTTCCCTGCAAGAACTGATGGCC 1320  
Db 1264 TTTTGGGCAATGCTCTAAGCTTCAAGCTTCCCTGCAAGAACTGATGGCC 1323  
QY 1321 TGAACCTCATCCCACTCTTGTATGACTCAAGTGTCAAGTCAATTTGTGATGAA 1380  
Db 1324 TGAACCTCATCCCACTCTTGTATGACTCAAGTGTCAAGTCAATTTGTGATGAA 1383  
QY 1381 CTGAATTAAGAACATCTTACGATATCAAGGAAACAGAAACAGAGATGGAAGGA 1440  
Db 1384 CTGAATTAAGAACATCTTACGATATCAAGGAAACAGAAACAGAGATGGAAGGA 1443  
QY 1441 CAGGAAGCAGCTTGGGACATTTAAAAATA 1472  
Db 1444 CAGGAAGCAGCTTGGGACATTTAAAAATA 1475  
  
RESULT 13  
AB188167  
ID AB188167 standard; cDNA; 1475 bp.  
XX  
AC AB188167;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO1356 cDNA sequence SEQ ID NO:191.  
XX  
KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive; vulnereary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.  
OS Homo sapiens.  
XX  
PN WO20020690-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 20-JUN-2001; 2001MO-US019692.  
XX  
XX 23-JUN-2000; 2000US-0213637P.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000MO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000MO-US023522.  
PR 24-AUG-2000; 2000MO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-0064610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000MO-US030952.  
PR 10-NOV-2000; 2000MO-US030873.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 20-DEC-2000; 2000US-00747259.







QY 841 TGGGTCGTGAAAAACAGTGGAGACAGACCCGAGGGCCACAGGTGAGGACACTACCACT 900  
DB 844 TGGGTCGTGAAAAACAGTGGAGACAGACCCGAGGGCCACAGGTGAGGACACTACCACT 903  
QY 901 GGATCGGTGAGAGGAGTGTCTGAGAGATGACTGACTTTGGCCATTGGATTGAGCAAG 960  
DB 904 GGATCGGTGAGAGGAGTGTCTGAGAGATGACTGACTTTGGCCATTGGATTGAGCAAG 963  
QY 961 GGAGAAATGGGGGCTACTGTATGACGATGACGATTTGAATTGGCAAGATCTGGCCATGC 1020  
DB 964 GGAGAAATGGGGGCTACTGTATGACGATGACGATTTGAATTGGCAAGATCTGGCCATGC 1023  
QY 1021 CAGGCTTTCTGTTTCTCTCACTGTGTCTCCCTGGCCCTTAAGTCCCAACCTCACTT 1080  
DB 1024 CAGGCTTTCTGTTTCTCTCACTGTGTCTCCCTGGCCCTTAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTCCTTAAGCCAGAGCTCAGAGATCCCTTGGCCCTTGGTTTAACTGGG 1140  
DB 1084 GAAACCCCATTCCTTAAGCCAGAGCTCAGAGATCCCTTGGCCCTTGGTTTAACTGGG 1143  
QY 1141 ACTTCATCCCAAAACCACTATATCAATCCCACTGACCTCTGTGATCAAAAGACC 1200  
DB 1144 ACTTCATCCCAAAACCACTATATCAATCCCACTGACCTCTGTGATCAAAAGACC 1203  
QY 1201 TCTCTCGGCGAGGTGGGCTTAAGCTCAATGTGGGGATGGGAGAGAGAGAGTGGG 1260  
DB 1204 TCTCTCGGCGAGGTGGGCTTAAGCTCAATGTGGGGATGGGAGAGAGAGTGGG 1263  
QY 1261 TTTTGTGGGCGATTGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1320  
DB 1264 TTTTGTGGGCGATTGCTTAACTTCTCAAGCTTCCCTCAAGAACTGATTGGCCC 1323  
QY 1321 TGGAACTTCATCCCACTCTTTGTTATGATCTCCAGAGTCCAGACTATTTTGTGATGA 1380  
DB 1324 TGGAACTTCATCCCACTCTTTGTTATGATCTCCAGAGTCCAGACTATTTTGTGATGA 1383  
QY 1381 CTGAAATTAATAACATCTTACGGTATCCAGGGAAGAGAGAGATCCAGATGGGAGGA 1440  
DB 1384 CTGAAATTAATAACATCTTACGGTATCCAGGGAAGAGAGAGATCCAGATGGGAGGA 1443  
QY 1441 CAGGAAGCAGGCTGGGACATTTAAAAAATA 1472  
DB 1444 CAGGAAGCAGGCTGGGACATTTAAAAAATA 1475

RESULT 15  
ABL95656 standard; cDNA; 1475 BP.  
ID ABL95656  
AC ABL95656;  
DT 19-JUL-2002 (first entry)  
DE Human angiogenesis related cDNA PRO1356 SEQ ID NO: 191.  
XX  
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;  
KW antiarteriosclerotic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO20020284-A2.  
XX  
PD 31-JAN-2002.  
XX  
PR 09-JUL-2001; 2001WO-US021735.  
XX  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220644P.  
PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-0064610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 22-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US065520.  
PR 01-MAR-2001; 2001WO-US066666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00834208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-0086028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX  
PA (GETH ) GENENTECH INC.  
PA (BAKE ) BAKER K P.  
PA (FERE ) FERRARA N.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODO ) GODDARD A.  
PA (GODO ) GODDARD P J.  
PA (GORN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (MARS ) MARSTERS S A.  
PA (PANU ) PAN J.  
PA (PAON ) PAONI N F.  
PA (STEP ) STEPHAN J P.  
PA (WATA ) WATAMBE C K.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Paoni NF, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watamabe CK, Williams PM, Wood WI, Ye W.  
XX  
XX WPI; 2002-171999/22.  
DR P-PSDB; ABB95518.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.  
XX  
PS Claim 1; Fig 191; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention  
CC  
CC Sequence 1475 BP; 345 A; 404 C; 376 G; 350 T; 0 U; 0 Other;



Query Match 53.78; Score 1472; DB 6; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGAGACTCTGAATAGAGGATAGAGTGTTCAGAGAGAGA 60  
DB 4 AGAAGTACGCTGGCAGAGAGACTCTGAATAGAGGATAGAGTGTTCAGAGAGAGA 63  
QY 61 GCTTACAGCTGAAGACAGAGAGAGAGTCCCTGAAGAGCTTCTAGAGAGTGTGCAT 120  
DB 64 GCTTACAGCTGAAGACAGAGAGAGAGTCCCTGAAGAGCTTCTAGAGAGTGTGCAT 123  
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTCTTGAGGCTTTTGGGAC 180  
DB 124 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTCTTGAGGCTTTTGGGAC 183  
QY 181 ACTGTTGGCAATGCTGTCTCCCAAGTGTGAAGAAAGTGTCTTAAATGCTGTGCTCCAGCATGT 240  
DB 184 ACTGTTGGCAATGCTGTCTCCCAAGTGTGAAGAAAGTGTCTTAAATGCTGTGCTCCAGCATGT 243  
QY 241 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTCACACAGACAGAGCAT 300  
DB 244 GACAGCAGTTGGCTTCTCAAGAGGCTCTGGATGGAATGTCACACAGACAGAGCAT 303  
QY 301 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 360  
DB 304 CACCCAGTGTGACATCTAAGACACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 363  
QY 361 GGCATATATGTGATCATCCAGTGAATCTCTCCCTGGCTGATCTTCTGTGGTGG 420  
DB 364 GGCATATATGTGATCATCCAGTGAATCTCTCCCTGGCTGATCTTCTGTGGTGG 423  
QY 421 CATGATGACAGAGTCTTCTGCCAGAAATCCGAGCCAAAGACAGATGGCGTGAAGG 480  
DB 424 CATGATGACAGAGTCTTCTGCCAGAAATCCGAGCCAAAGACAGATGGCGTGAAGG 483  
QY 481 TGAAGTCTTTTCAATCCTTGAGAGGCTCTGGAGATTCATTCCTGTGCTTGAATCTTCA 540  
DB 484 TGAAGTCTTTTCAATCCTTGAGAGGCTCTGGAGATTCATTCCTGTGCTTGAATCTTCA 543  
QY 541 TGGGATCTTACGAGGACTTCTAATCAACATGTGTGCTGACAGCATGAAATTTGAGATTGG 600  
DB 544 TGGGATCTTACGAGGACTTCTAATCAACATGTGTGCTGACAGCATGAAATTTGAGATTGG 603  
QY 601 AGAGGCTCTTCACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATCT 660  
DB 604 AGAGGCTCTTCACTTGGGCAATTAATTTCTCCCTGTCTCCCTGATAGCTGGAATCATCT 663  
QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGTCCAACTACATGATGCTCAAGGCCA 720  
DB 664 CTGCTTTCTGCTCATCCAGAGAAATCGTCCAACTACATGATGCTCAAGGCCA 723  
QY 721 ACTCTTGGCAAGAGAGCTCTCAAGGCTGTGCAACTTCCAAATCAAGATGAGTT 780  
DB 724 ACTCTTGGCAAGAGAGCTCTCAAGGCTGTGCAACTTCCAAATCAAGATGAGTT 783  
QY 781 CAATTCCTACAGCCTGACAGGATATGTGTAAGAACAGGGGSCCAGAGCTGGGGGCTGGC 840  
DB 784 CAATTCCTACAGCCTGACAGGATATGTGTAAGAACAGGGGSCCAGAGCTGGGGGCTGGC 843  
QY 841 TGGGCTGTGTAAGAAACAGTGAACAGACCCCGAGGGCCACAGGTGAGGAGACATCACT 900  
DB 844 TGGGCTGTGTAAGAAACAGTGAACAGACCCCGAGGGCCACAGGTGAGGAGACATCACT 903  
QY 901 GGATCTGTGTAAGAGGCTGTGCTGAGATGACATCTTGGGCTTGGATTTGAGCAAG 960  
DB 904 GGATCTGTGTAAGAGGCTGTGCTGAGATGACATCTTGGGCTTGGATTTGAGCAAG 963  
QY 961 GCAGAAATGGGGGCTAGGTGAACAGATGACAGTTGAATTGCCAAGGATGCTGSCCATGC 1020  
DB 964 GCAGAAATGGGGGCTAGGTGAACAGATGACAGTTGAATTGCCAAGGATGCTGSCCATGC 1023  
QY 1021 CAGCCTTCTGTCTTCTCACTTGTGCTGCCCTGACCTTAAGTCCCAACCTCACTT 1080

DB 1024 CAGCCTTCTGTCTTCTCACTTGTGCTGCCCTTAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTGTGATTAAGTGGG 1140  
DB 1084 GAAACCCATTCCTTAAAGCAGAGACTCAGAGAGATCCCTTGGCTGTGATTAAGTGGG 1143  
QY 1141 ACTCATCCCAACCCCACTAATCAATCCCACTGACCTGATGATCAAGAACCC 1200  
DB 1144 ACTCATCCCAACCCCACTAATCAATCCCACTGACCTGATGATCAAGAACCC 1203  
QY 1201 TCTCTGTGAGTGTGGCTCTTAAGTCTTGTGATGATGAGAGAGAGAGAGTGGC 1260  
DB 1204 TCTCTGTGAGTGTGGCTCTTAAGTCTTGTGATGATGAGAGAGAGAGAGTGGC 1263  
QY 1261 TTTTGTGGGATGTCTTAAGTCTTCAAGCTTCCCTCCAAAGAACTGATTTGGCC 1320  
DB 1264 TTTTGTGGGATGTCTTAAGTCTTCAAGCTTCCCTCCAAAGAACTGATTTGGCC 1323  
QY 1321 TGGAACTTCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1380  
DB 1324 TGGAACTTCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1383  
QY 1381 CTGAATTAAGACATCTTAAGGATTCAGAGAACAGAAAGCAGATGAGATGGAGGA 1440  
DB 1384 CTGAATTAAGACATCTTAAGGATTCAGAGAACAGAAAGCAGATGAGATGGAGGA 1443  
QY 1441 CAGAAAGCAGCCTGGGACATTTAAATAATA 1472  
DB 1444 CAGAAAGCAGCCTGGGACATTTAAATAATA 1475

Search completed: October 30, 2004, 18:35:59  
Job time : 1851 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 15:35:31 ; Search time 293 Seconds  
(without alignments)  
6651.820 Million cell updates/sec

Title: US-09-787-677a-7  
Perfect score: 2742  
Sequence: 1 agagtcagcctgcgcagaga.....gtcgtacataatcgtacg 2742

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 20

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: \*  
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6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472	53.7	1475	US-10-140-002-491	Sequence 491, App
2	1291	47.1	1400	US-09-663-600A-139	Sequence 139, App
3	896	32.7	1524	US-09-663-600A-45	Sequence 45, App1
4	20	0.7	1485	US-09-113-000C-1944	Sequence 1944, App
5	20	0.7	13930	US-09-976-594-1011	Sequence 1011, App
6	20	0.7	13993	US-09-220-132-20	Sequence 20, App1
7	20	0.7	14070	US-09-108-006C-2	Sequence 2, App1
8	20	0.7	1664976	US-08-916-421B-1	Sequence 1, App1
9	20	0.7	1664976	US-09-692-570-1	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-10-140-002-491  
Sequence 491, Application US/10140002  
Patent No. 6725730  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OR INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C59  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 491  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-002-491

Query Match 53.7%; Score 1472; DB 4; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGAAGTCAGCCTGGCAGAGAGACTTGAATAGAGATTAGAGTGTTCAGAGAGAGAGA	60
DB	4	AGAAGTCAGCCTGGCAGAGAGAGACTTGAATAGAGATTAGAGTGTTCAGAGAGAGAGA	63
QY	61	GCTTTCAGCCTGGAAG	120
DB	64	GCTTTCAGCCTGGAAG	123
QY	121	GCGCTCTCTTGGCTTCCAACTTTGGGCTTACATCTTACATCTTACATCTTACATCTT	180
DB	124	GCGCTCTCTTGGCTTCCAACTTTGGGCTTACATCTTACATCTTACATCTTACATCTT	183
QY	181	ACTGTTGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
DB	184	ACTGTTGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	243
QY	241	GACAGCAGTGGCTTCTCCAGAGGAGCTCTGATGATGATGATGATGATGATGATGATG	300
DB	244	GACAGCAGTGGCTTCTCCAGAGGAGCTCTGATGATGATGATGATGATGATGATGATG	303
QY	301	CACCCAGTGTGATCTATATGACACCTTCTGGGCTTGGGCTTGGGCTTGGGCTTGGG	360
DB	304	CACCCAGTGTGATCTATATGACACCTTCTGGGCTTGGGCTTGGGCTTGGGCTTGGG	363
QY	361	GCGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	420
DB	364	GCGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	423
QY	421	CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	480
DB	424	CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	483
QY	481	TGAGTCTTTTCACTTGAAGGCTCTGGAATTCATCTTCTGTTCTCTGGAATCTTCA	540
DB	484	TGAGTCTTTTCACTTGAAGGCTCTGGAATTCATCTTCTGTTCTCTGGAATCTTCA	543
QY	541	TGGATTCCTTACCGGATCTTCACTCAACATGAGGCTGAGCAGATGAAATTTGAGATTG	600
DB	544	TGGATTCCTTACCGGATCTTCACTCAACATGAGGCTGAGCAGATGAAATTTGAGATTG	603
QY	601	AGAAGCTCTTAACTTGGGATTTTCTTCTCTGTTCTCTGTTCTCTGTTCTCTGTTCT	660
DB	604	AGAAGCTCTTAACTTGGGATTTTCTTCTCTGTTCTCTGTTCTCTGTTCTCTGTTCT	663
QY	661	CTGCTTTCTGCTCATCCAGAGAAATGCTTCACTTACATGATGATGATGATGATGATG	720
DB	664	CTGCTTTCTGCTCATCCAGAGAAATGCTTCACTTACATGATGATGATGATGATGATG	723

QY 721 ACCTCTTGCCAGAGAGCTCTCCAGAGCCTGTGCAACCTCCCAAGTCAAGAGTGT 780  
DB 724 ACCTCTTGCCAGAGAGCTCTCCAGAGCCTGTGCAACCTCCCAAGTCAAGAGTGT 783  
QY 781 CAATCTCTACAGCTGACAGAGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 840  
DB 784 CAATCTCTACAGCTGACAGAGGTATGTGTGAAGAACAGAGGGCCAGAGCTGGGGGGTGGC 843  
QY 841 TGGGCTCTGTGAAGAACAGTGGACAGACCCGAGAGGACAGAGTGAAGGACATCACTACT 900  
DB 844 TGGGCTCTGTGAAGAACAGTGGACAGACCCGAGAGGACAGAGTGAAGGACATCACTACT 903  
QY 901 GATCTGTCTCAAGAGAGTGTCTGTAGAGATAGACTTGTGGCCATTGATTGAAGCAAG 960  
DB 904 GATCTGTCTCAAGAGAGTGTCTGTAGAGATAGACTTGTGGCCATTGATTGAAGCAAG 963  
QY 961 GCAGAAATGGGGGGCTAGTGTGAAGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020  
DB 964 GCAGAAATGGGGGGCTAGTGTGAAGAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1023  
QY 1021 CAGGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1080  
DB 1024 CAGGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1083  
QY 1081 GAAACCCCATTTCCCTTAAGCCAGAGACTCAAGAGATCCCTTGTGCTTGAACCTGGG 1140  
DB 1084 GAAACCCCATTTCCCTTAAGCCAGAGACTCAAGAGATCCCTTGTGCTTGAACCTGGG 1143  
QY 1141 ACTTCATCCCAAG 1200  
DB 1144 ACTTCATCCCAAG 1203  
QY 1201 TCTCTGTGCTGAGAGTGTGCTGTAGCTCATTTGTGGGAGATGGAGAGAGAGAGAGAGAG 1260  
DB 1204 TCTCTGTGCTGAGAGTGTGCTGTAGCTCATTTGTGGGAGATGGAGAGAGAGAGAGAGAG 1263  
QY 1261 TTTTGTGGGAGATTTGCTTAACCTTCTCTCAAGCTTCCCTCAAGAGAGAGAGAGAGAGAG 1320  
DB 1264 TTTTGTGGGAGATTTGCTTAACCTTCTCTCAAGCTTCCCTCAAGAGAGAGAGAGAGAGAG 1323  
QY 1321 TGAAGCTCCATCCCACTCTTGTGTATGATCTCAAGAGTGTCAAGCTTAATTTGTGAGAA 1380  
DB 1324 TGAAGCTCCATCCCACTCTTGTGTATGATCTCAAGAGTGTCAAGCTTAATTTGTGAGAA 1383  
QY 1381 CTGAATTAAGAACATCTCTAGGTATCCAGAGAGAGAGAGAGAGAGATGAGATGGAGAG 1440  
DB 1384 CTGAATTAAGAACATCTCTAGGTATCCAGAGAGAGAGAGAGAGATGAGATGGAGAG 1443  
QY 1441 CAGGAGGAGAGCTGTGAGACATTTAAATAATA 1472  
DB 1444 CAGGAGGAGAGCTGTGAGACATTTAAATAATA 1475

RESULT 2  
US-09-663-600A-139  
Sequence 139, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bouquelaret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121

QY 84 CATTCCTTAAGAGAGCTTCTCACTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 143  
DB 1 CATTCCTTAAGAGAGCTTCTCACTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 60  
QY 144 TGGGCTACATCTCAGAGAGCTTCTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 203  
DB 61 TGGGCTACATCTCAGAGAGCTTCTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 120  
QY 204 GCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 263  
DB 121 GCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 180  
QY 264 GCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 323  
DB 181 GCTGAGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTG 240  
QY 324 CCCTTCTGAG 383  
DB 241 CCCTTCTGAG 300  
QY 384 CAATCT 443  
DB 301 CAATCT 360  
QY 444 AGGAATCCGAG 503  
DB 361 AGGAATCCGAG 420  
QY 504 GCTCTGAG 563  
DB 421 GCTCTGAG 480  
QY 564 CACCACTGTGCTGACAGAGATGAATTTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623  
DB 481 CACCACTGTGCTGACAGAGATGAATTTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 624 TTTCTTCT 683  
DB 541 TTTCTTCT 600  
QY 684 GAAATGCTCACTACTAG 743  
DB 601 GAAATGCTCACTACTAG 660

Query Match 47.1%; Score 1291; DB 4; Length 1400;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1391; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	744	CAAGGCCGTGCACACTCCCAAAGTCAGAGTGAGTTCAATTCCATCAGCCCTGACAGGGT	803
Db	661	CAAGGCCGTGCACACTCCCAAAGTCAGAGTGAGTTCAATTCCATCAGCCCTGACAGGGT	720
QY	804	ATGTGTGAAGAAACAAGGGGCCAGAGCTGGGGGGGTGGCTGGGTCTGTGTGAAAAACAGTGGAC	863
Db	721	ATGTGTGAAGAAACAAGGGGCCAGAGCTGGGGGGGTGGCTGGGTCTGTGTGAAAAACAGTGGAC	780
QY	864	AGCACCCCGAGGGCCACAGGTGAGGGACACTACCTGATGTGTCTAGAAAGTGTGCT	923
Db	781	AGCACCCCGAGGGCCACAGGTGAGGGACACTACCTGATGTGTCTAGAAAGTGTGCT	840
QY	924	GAGGATGACCTGACTTTTGGCCATTGGATTGAGCAAAAGCACAATAATGGGGGGCTAGGTGAC	983
Db	841	GAGGATGACCTGACTTTTGGCCATTGGATTGAGCAAAAGCACAATAATGGGGGGCTAGGTGAC	900
QY	984	AGCATGACAGTGTGAATTCCAAAGATGCTCCGACATGCCAGCCCTTCTGTCTTCCCTCACT	1043
Db	901	AGCATGACAGTGTGAATTCCAAAGATGCTCCGACATGCTCCGACATGCTTCTGTCTTCCCTCACT	960
QY	1044	TGCTGTCTCCCTGTGCTTAAGTTCGCCCAACCTCTCAACTTGAAAACCCCATTTCCCTTAAAGCAG	1103
Db	961	TGCTGTCTCCCTGTGCTTAAGTTCGCCCAACCTCTCAACTTGAAAACCCCATTTCCCTTAAAGCAG	1020
QY	1104	GACTCAGAGGATCCCTTTGGCCCTGTGCTTTACCTGGGACTGCATCCTCCCAAACCCACTAAT	1163
Db	1021	GACTCAGAGGATCCCTTTGGCCCTGTGCTTTACCTGGGACTGCATCCTCCCAAACCCACTAAT	1080
QY	1164	CACATCCCACTGACTGACCTCTCTGTGATCAAAAGACCTCTCTCTGGCTGAGGTGGCTCT	1223
Db	1081	CACATCCCACTGACTGACCTCTCTGTGATCAAAAGACCTCTCTCTGGCTGAGGTGGCTCT	1140
QY	1224	TAGCTCATTTGCTGGGATGGAGAGGAAGACAGTGGCTTTTGTGAGGCAATTGCTCTTAACCT	1283
Db	1141	TAGCTCATTTGCTGGGATGGAGAGGAAGACAGTGGCTTTTGTGAGGCAATTGCTCTTAACCT	1200
QY	1284	ACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCCTGGAACTCCATCCACTCTTGT	1343
Db	1201	ACTTCTCAAGCTTCCCTCCAAAGAACTGATTTGGCCCTGGAACTCCATCCACTCTTGT	1260
QY	1344	TATGACTCCACAGTGTCCAGACTAATTTGTGCATGACCTGAATTAACATCTTAAGGT	1403
Db	1261	TATGACTCCACAGTGTCCAGACTAATTTGTGCATGACCTGAATTAACATCTTAAGGT	1320
QY	1404	ATCCAGGGAACAGAAAGCAGATGACGATGGGAGACAGAAAGGCACTGGGACATTT	1463
Db	1321	ATCCAGGGAACAGAAAGCAGATGACGATGGGAGACAGAAAGGCACTGGGACATTT	1380
QY	1464	AAAAAAAAATAAAA 1476	
Db	1381	AAAAAAAAATAAAA 1393	
RESULT 3			
US-09-663-600A-45			
; Sequence 45, Application US/09663600A			
; Patent No. 6573068			
; GENERAL INFORMATION:			
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste			
; APPLICANT: Duclert, Aymeric			
; APPLICANT: Bougueleret, Lydie			
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS			
; FILE REFERENCE: 31.US3.CIP			
; CURRENT APPLICATION NUMBER: US/09/663, 600A			
; CURRENT FILING DATE: 2000-09-15			
; PRIOR APPLICATION NUMBER: 09/191, 997			
; PRIOR FILING DATE: 1998-11-13			
; PRIOR APPLICATION NUMBER: 60/066, 677			
; PRIOR FILING DATE: 1997-11-13			
; PRIOR APPLICATION NUMBER: 60/069, 957			
; PRIOR FILING DATE: 1997-12-17			
; PRIOR APPLICATION NUMBER: 60/074, 121			
; PRIOR FILING DATE: 1998-02-09			

Query Match	Best Local Similarity	Score	DB 4	Length	1524
Matches 1046; Conservative	99.78;	0;	Mismatches	3;	Indels
					Gaps
					0
57	AAAGCTTCACCTCGAAGACAAGGAGACAGTCCCTGAAAGACGCTTCTACTGAGAGCTG	116			
98	AAAGCTTCACCTCGAAGACAAGGAGACAGTCCCTGAAAGACGCTTCTACTGAGAGCTG	157			
117	CCATGGCTCTCTTGGGCTCCAACTTGTGGGCTACATCTNAGGCTTCTGGGGCTTTTGG	176			
158	CCATGGCTCTCTTGGGCTCCAACTTGTGGGCTACATCTNAGGCTTCTGGGGCTTTTGG	217			
177	GCATACGTGTTCCATGTGTCTCCCACTGTGAAACAAAGTTTATGTCCGTGCACAA	236			



ORGANISM: Homo sapiens  
US-09-220-132-20

Query Match 0.7%; Score 20; DB 4; Length 13993;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2104 CATATCCATGCCACGGTGC 2123  
DB 1203 CATATCCATGCCACGGTGC 12020

RESULT 7  
US-09-108-006C-2/c  
Sequence 2, Application US/09108006C  
Patent No. 6524613  
GENERAL INFORMATION:  
APPLICANT: Steer, Clifford J.  
Kren, Betsy T.  
Bandopadhyay, Paramita  
Roy-Chowdhury, Jayanta  
TITLE OF INVENTION: Hepatocellular Chimeraplasty  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kimeragen, Inc.  
STREET: 300 Pleasant Run  
CITY: Newtown  
STATE: PA  
COUNTRY: USA  
ZIP: 18940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108, 006C  
FILING DATE: 30-Jun-1992  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,288  
FILING DATE: 30-APR-1997  
APPLICATION NUMBER: 60/054,837  
FILING DATE: 05-AUG-1997  
APPLICATION NUMBER: 60/064,996  
FILING DATE: 10-NOV-1997  
APPLICATION NUMBER: 60/074,497  
FILING DATE: 12-FEB-1998  
APPLICATION NUMBER: PCT US 98/08834  
FILING DATE: 30-APR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Fiedel, Thomas  
REGISTRATION NUMBER: 29258  
REFERENCE/DOCKET NUMBER: 7991-015-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-504-4444  
TELEFAX: 215-504-4545  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14070 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-108-006C-2

Query Match 0.7%; Score 20; DB 4; Length 14070;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2104 CATATCCATGCCACGGTGC 2123  
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DB 12117 CATATCCATGCCACGGTGC 12098

RESULT 8  
US-08-916-421B-1  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Built et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
Patent No. 6503729  
FILE REFERENCE: PB275  
CURRENT APPLICATION NUMBER: US/08/916,421B  
CURRENT FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
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US-08-916-421B-1

Query Match 0.7%; Score 20; DB 4; Length 1664976;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 ACATTAAATAATAATAAT 1477  
Db 1221630 ACATTAAATAATAATAAT 1221649

RESULT 9  
US-09-692-570-1  
Sequence 1, Application US/09692570  
Patent No. 6797466  
GENERAL INFORMATION:  
APPLICANT: Bult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
Patent No. 6797466  
TITLE OF INVENTION: jannaschii  
FILE REFERENCE: PB275C1  
CURRENT APPLICATION NUMBER: US/09/692,570  
CURRENT FILING DATE: 2003-01-14  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
PRIOR APPLICATION NUMBER: US 08/916,421  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii  
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LOCATION: (28222)..(28222)  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1221630 ACATTAAAAAATAAAAAT 1221649

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Search completed: October 30, 2004, 13:22:06  
Job time : 298 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 01:21:03 ; Search time 1793 Seconds  
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Title: US-09-787-677a-7  
Perfect score: 2742  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3413475 seqs, 2563800928 residues

Word size : 20

Total number of hits satisfying chosen parameters: 816

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2513	91.6	2863	15 US-10-301-822-23	Sequence 23, Appl
2	1472	53.7	1475	10 US-09-888-257A-1	Sequence 1, Appl
3	1472	53.7	1475	10 US-09-946-374-133	Sequence 133, App
4	1472	53.7	1475	13 US-10-006-867-79	Sequence 79, Appl
5	1472	53.7	1475	13 US-10-063-547-79	Sequence 79, Appl
6	1472	53.7	1475	13 US-10-063-551-79	Sequence 79, Appl
7	1472	53.7	1475	14 US-10-028-072-491	Sequence 491, App
8	1472	53.7	1475	14 US-10-063-616-79	Sequence 79, Appl
9	1472	53.7	1475	14 US-10-140-808-491	Sequence 491, App
10	1472	53.7	1475	14 US-10-063-569-79	Sequence 79, Appl
11	1472	53.7	1475	14 US-10-063-513-79	Sequence 79, Appl
12	1472	53.7	1475	14 US-10-063-515-79	Sequence 79, Appl

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33	1472	53.7	1475	14 US-10-142-423-491	Sequence 491, App
34	1472	53.7	1475	14 US-10-063-598-79	Sequence 79, Appl
35	1472	53.7	1475	14 US-10-227-693-79	Sequence 79, Appl
36	1472	53.7	1475	14 US-10-006-818A-133	Sequence 133, App
37	1472	53.7	1475	14 US-10-121-050-491	Sequence 491, App
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45	1472	53.7	1475	14 US-10-063-594-79	Sequence 79, Appl

#### ALIGNMENTS

RESULT 1  
US-10-301-822-23  
Sequence 23, Application US/10301822  
Publication No. US20030148410A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kamatkar, Shubhangt  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John R.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MEMO1-029P22NM  
CURRENT APPLICATION NUMBER: US/10/301,822  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 2863  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (231)...(923)  
US-10-301-822-23

Query Match 91.6%; Score 2513; DB 15; Length 2863;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2713; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAGAGGTCTTCAAGAGCAAGA 60  
DB 113 AGAAGTCAGCTGGCAGAGAGACTCTGAATGAGGATTAGAGGTCTTCAAGAGCAAGA 172  
QY 61 GCTTACAGCTGGAAGCAAGGAGAGAGCTCCGTAAGAGAGCTTCTAAGAGGTCTGCAT 120  
DB 173 GCTTACAGCTGGAAGCAAGGAGAGAGCTCCGTAAGAGAGCTTCTAAGAGGTCTGCAT 232  
QY 121 GGGCTCTCTTGGCTCCCACTTGTGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 180  
DB 233 GGGCTCTCTTGGCTCCCACTTGTGGCTACATCTAGAGCTTCTGGGGCTTTTGGGAC 292  
QY 181 ACTGTTGCCATGTCTCTCCAGCTGGAAGCAAGTTCTTATGTGGTGCAGCATTTGT 240  
DB 293 ACTGTTGCCATGTCTCTCCAGCTGGAAGCAAGTTCTTATGTGGTGCAGCATTTGT 352  
QY 241 GACAGCAGTTGGGCTTCTCAAGGGGCTCTGGATGGAATGTGCCACACAGCAGGAGAT 300  
DB 353 GACAGCAGTTGGGCTTCTCAAGGGGCTCTGGATGGAATGTGCCACACAGCAGGAGAT 412  
QY 301 CACCCAGTGTGACATCTATAGCACTCTTGGGCTGCGCCGCTGACATCCAGGCTGCCA 360  
DB 413 CACCCAGTGTGACATCTATAGCACTCTTGGGCTGCGCCGCTGACATCCAGGCTGCCA 472  
QY 361 GGGCATAATGATGACATCCAGTGCATCTCTCTGCTGGCTGCTATATCTGTGTGGG 420  
DB 473 GGGCATAATGATGACATCCAGTGCATCTCTCTGCTGGCTGCTATATCTGTGTGGG 532  
QY 421 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAGAAAGACAGATGGCGGTAGCAG 480  
DB 533 CATGAGATGACAGTCTTCTGCCAGAAATCCGAGCCAGAAAGACAGATGGCGGTAGCAG 592  
QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTTCAATTCCTGTGCTTGAATCTTCA 540  
DB 593 TGAAGTCTTTTCAATCTTGAAGGCTCTGGGATTTCAATTCCTGTGCTTGAATCTTCA 652  
QY 541 TGGGATCTTACGGGACTTCTTACTACACATGTGTGCTGACAGCATGAAATTTGAGTTGG 600  
DB 653 TGGGATCTTACGGGACTTCTTACTACACATGTGTGCTGACAGCATGAAATTTGAGTTGG 712  
QY 601 AGAGGCTCTTCACTTGGGCAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 713 AGAGGCTCTTCACTTGGGCAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772  
QY 661 CTGCTTTCTCTGCTCATCCAGAGAAATCGCTCCACTTACGATGCTACCAAGCCCA 720  
DB 773 CTGCTTTCTCTGCTCATCCAGAGAAATCGCTCCACTTACGATGCTACCAAGCCCA 832  
QY 721 ACCTCTTGGCAAGAGGCTCTCCAGAGCTGTGCTCAACCTTCCCAATGCAAGTGTGTT 780  
DB 833 ACCTCTTGGCAAGAGGCTCTCCAGAGCTGTGCTCAACCTTCCCAATGCAAGTGTGTT 892  
QY 781 CAATTCCTACAGCTGACAGGATGTGTGAAGAACAGAGGAGCCAGAGCTGGGGGGTGGC 840  
DB 893 CAATTCCTACAGCTGACAGGATGTGTGAAGAACAGAGGAGCCAGAGCTGGGGGGTGGC 952  
QY 841 TGGGCTCTGTGAAGAACAGTGCAGCACCAGAGGAGCCAGAGTGCAGTGCAGTGCAGTGC 900  
DB 953 TGGGCTCTGTGAAGAACAGTGCAGCACCAGAGGAGCCAGAGTGCAGTGCAGTGCAGTGC 1012  
QY 901 GGAATCTGTGACAGAGGCTGTGCTGAGATGACATCTTGGCCATTGATGAGCAAG 960  
DB 1013 GGAATCTGTGACAGAGGCTGTGCTGAGATGACATCTTGGCCATTGATGAGCAAG 1072  
QY 961 GCAAGAAATGGGGGCTAGGTATACAGCATGAGTGAATGCCAAGAGTGTGCGCATGCG 1020  
DB 1073 GCAAGAAATGGGGGCTAGGTATACAGCATGAGTGAATGCCAAGAGTGTGCGCATGCG 1132

QY 1021 CAGCCTTTCTGTCTTCTCACTTGTCTGCTCCCTGCTGCTTAACTGCCCAACCTCAACTT 1080  
DB 1133 CAGCCTTTCTGTCTTCTCACTTGTCTGCTCCCTGCTGCTTAACTGCCCAACCTCAACTT 1192  
QY 1081 GAAACCCCAATTCCTTAAGCAGAGACTCAGAGAGATCCCTTGGCCCTGAGTTTAACTGGG 1140  
DB 1193 GAAACCCCAATTCCTTAAGCAGAGACTCAGAGAGATCCCTTGGCCCTGAGTTTAACTGGG 1252  
QY 1141 ACTCAATCCCAAAACCACTAATCAATCCCACTGACCTGCTGTGATCAAGAACCC 1200  
DB 1253 ACTCAATCCCAAAACCACTAATCAATCCCACTGACCTGCTGTGATCAAGAACCC 1312  
QY 1201 TCTCTGCTGAGGTTGGTGTCTTACTGATTTGCTGGGATGGGAAAGAGACAGTGGC 1260  
DB 1313 TCTCTGCTGAGGTTGGTGTCTTACTGATTTGCTGGGATGGGAAAGAGACAGTGGC 1372  
QY 1261 TTTTGGGGGATGTGCTAATCCACTTCTCAAGCTTCCCTGCAAGAACTGATTTGGGCC 1320  
DB 1373 TTTTGGGGGATGTGCTAATCCACTTCTCAAGCTTCCCTGCAAGAACTGATTTGGGCC 1432  
QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1380  
DB 1433 TGGAACTCCATCCCACTCTCTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGAA 1492  
QY 1381 CTGAAATTAAGCACTCTTACGGTATCCAGGAAACAGAAAGCAGATGCGAGTGGAGGA 1440  
DB 1493 CTGAAATTAAGCACTCTTACGGTATCCAGGAAACAGAAAGCAGATGCGAGTGGAGGA 1552  
QY 1441 CAGAAAGGAGCAGCTGGGACATTTAAATAATTAATAATTAATAATTAATAATTAATAAT 1500  
DB 1553 CAGAAAGGAGCAGCTGGGACATTTAAATAATTAATAATTAATAATTAATAATTAATAAT 1612  
QY 1501 TCTCAAGGGCACTTTCAGAAATCTCTCAATTTGTGGGCTGGGATCAAGCTTGCAGCTTG 1560  
DB 1613 TCTCAAGGGCACTTTCAGAAATCTCTCAATTTGTGGGCTGGGATCAAGCTTGCAGCTTG 1672  
QY 1561 AGGAAAGCAGAGAAAGAAAGAAAGAAATCTGTGTGAAGAGCTCAGGTGGCAGCGGACTCTG 1620  
DB 1673 AGGAAAGCAGAGAAAGAAAGAAAGAAATCTGTGTGAAGAGCTCAGGTGGCAGCGGACTCTG 1732  
QY 1621 ACTCACTGAGGAACTGCTCAGAGCTGAGATCAGAACTTTGGGCTGAAAGCCCTGCTC 1680  
DB 1733 ACTCACTGAGGAACTGCTCAGAGCTGAGATCAGAACTTTGGGCTGAAAGCCCTGCTC 1792  
QY 1681 ACTCTAGGGGCACTTGCCTGCTGCTTAAACCAAGGCTTAAAGGCTAATGCAAT 1740  
DB 1793 ACTCTAGGGGCACTTGCCTGCTGCTTAAACCAAGGCTTAAAGGCTAATGCAAT 1852  
QY 1741 GGTTCCTTAAGAACTGTAACAGTAACTAGTTTCTTGAAGGATGGCCCTGCGGGGATGACA 1800  
DB 1853 GGTTCCTTAAGAACTGTAACAGTAACTAGTTTCTTGAAGGATGGCCCTGCGGGGATGACA 1912  
QY 1801 GTGTGGAGGCTGTGGGATCTGAGAAAGACCACTTCTTGAAGGATGGCCCTGCGGGGATGACA 1860  
DB 1913 GTGTGGAGGCTGTGGGATCTGAGAAAGACCACTTCTTGAAGGATGGCCCTGCGGGGATGACA 1972  
QY 1861 GTGATGT 1920  
DB 1973 GTGATGT 2032  
QY 1921 AGAAATCTTCAAGGCTAATGAAATCACTAATGAGATGAGGCTCCCAAGGCTGC 1980  
DB 2033 AGAAATCTTCAAGGCTAATGAAATCACTAATGAGATGAGGCTCCCAAGGCTGC 2092  
QY 1981 ACCCAGAGGCACTTACAGAGCTCTGAAAGACATGACCAAGGAGGCTTGCAGATT 2040  
DB 2093 ACCCAGAGGCACTTACAGAGCTCTGAAAGACATGACCAAGGAGGCTTGCAGATT 2152  
QY 2041 CCCCCTGTCTCATTCGAAAGATGCTCCAGAGTGTGTGAGGAGGCTTAAAGGCTCCAGCA 2100  
DB 2153 CCCCCTGTCTCATTCGAAAGATGCTCCAGAGTGTGTGAGGAGGCTTAAAGGCTCCAGCA 2212  
QY 2101 TGGCATATCCATGCCACGGT 2160



QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGCTCAACTAGATGCTTCAACCAAGCCCA 720  
DB 664 CTGCTTTCTGCTCATCCAGAGAAATCGCTCAACTAGATGCTTCAACCAAGCCCA 723  
QY 721 ACCCTTGGCAAGAGGCTCTCCAAAGGCTGGTCACTCCCAAGTCAAGAGTGT 780  
DB 724 ACCCTTGGCAAGAGGCTCTCCAAAGGCTGGTCACTCCCAAGTCAAGAGTGT 783  
QY 781 CAATTCCTAGAGCTGACAGGCTATGTGTGAAGAACAGAGGAGGAGAGTGGGGTGGC 840  
DB 784 CAATTCCTAGAGCTGACAGGCTATGTGTGAAGAACAGAGGAGGAGAGTGGGGTGGC 843  
QY 841 TGGGCTGTGAAAAACAGTGAACGACACCCGAGGAGGACAGGTTGAGGACACTACT 900  
DB 844 TGGGCTGTGAAAAACAGTGAACGACACCCGAGGAGGACAGGTTGAGGACACTACT 903  
QY 901 GGAATCGGTGAGAAAGGTGCTGAGAGATGACTGACTTGGCCATTGGAATTGAGCAAG 960  
DB 904 GGAATCGGTGAGAAAGGTGCTGAGAGATGACTGACTTGGCCATTGGAATTGAGCAAG 963  
QY 961 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATTGCCAAGAGTCTGCCATGC 1020  
DB 964 GCAGAAATGGGGGCTAGTGTAAACAGATGACAGGTTGAATTGCCAAGAGTCTGCCATGC 1023  
QY 1021 CAGCCTTTCTGTTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCAACTT 1080  
DB 1024 CAGCCTTTCTGTTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCAACTT 1083  
QY 1081 GAAACCCCATTCCTCTTAAGCAGAGACTCAAGAGATTCCTTGGCTGTTAACTGGG 1140  
DB 1084 GAAACCCCATTCCTCTTAAGCAGAGACTCAAGAGATTCCTTGGCTGTTAACTGGG 1143  
QY 1141 ACTTCATCCCAACCACTAATCAATCCCACTGACCTCTGTGTAAAGAACCC 1200  
DB 1144 ACTTCATCCCAACCACTAATCAATCCCACTGACCTCTGTGTAAAGAACCC 1203  
QY 1201 TCTCTGTGCTGAGTGGTCTTAACTCAATGCTGGGAGTGGAGAGAGAGAGTGGC 1260  
DB 1204 TCTCTGTGCTGAGTGGTCTTAACTCAATGCTGGGAGTGGAGAGAGAGAGTGGC 1263  
QY 1261 TTTTGTGGGAGTGGCTTAACTCAATGCTGGGAGTGGAGAGAGAGAGTGGC 1320  
DB 1264 TTTTGTGGGAGTGGCTTAACTCAATGCTGGGAGTGGAGAGAGAGAGTGGC 1323  
QY 1321 TGGAACTTCATCCCACTCTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1380  
DB 1324 TGGAACTTCATCCCACTCTTGTATGACTCAAGTGTCCAGACTAATTTGTGATGAA 1383  
QY 1381 CTGAATTAACCACTCTTACGGTATCCAGAGAACAGAAAGCAGATGAGAGAGGA 1440  
DB 1384 CTGAATTAACCACTCTTACGGTATCCAGAGAACAGAAAGCAGATGAGAGAGGA 1443  
QY 1441 CAGGAGGAGGCTGGGAGCAATTTAAAAATA 1472  
DB 1444 CAGGAGGAGGCTGGGAGCAATTTAAAAATA 1475

## RESULT 3

US-09-946-374-133  
Sequence 133, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
APPLICANT: Bacon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
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PRIOR FILING DATE: 1998-09-02  
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PRIOR APPLICATION NUMBER: 60/102307  
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PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
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PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314

PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
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PRIOR FILING DATE: 1998-10-08  
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PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 53.7%; Score 1472; DB 10; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGAGACTTGAATGAGGATTAGAGTGTCAAGAGCAAGA 60  
DB 4 AGAAGTACGCTGGCAGAGAGACTTGAATGAGGATTAGAGTGTCAAGAGCAAGA 63  
QY 61 GCTTACGCTGAAGAGCAAGGAGAGAGCTTGAAGAGCTTCTAAGAGAGTCTGCAT 120  
DB 64 GCTTACGCTGAAGAGCAAGGAGAGAGCTTGAAGAGCTTCTAAGAGAGTCTGCAT 123  
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGCTACATCTAGGCTTCTGAGGCTTTGGGAC 180  
DB 124 GGCCTCTCTTGGCCTCCAACTTGTGGCTACATCTAGGCTTCTGAGGCTTTGGGAC 183  
QY 181 ACTGTTGCGATGCTGTCTCCAGCTGGAAGAAAGTCTTATGTGCTGCCAGCATTT 240  
DB 184 ACTGTTGCGATGCTGTCTCCAGCTGGAAGAAAGTCTTATGTGCTGCCAGCATTT 243  
QY 241 GACAGAGTGGCTTCTCCAAAGGAGCTTGGATGGAATGTGCCACACAGAGCAT 300  
DB 244 GACAGAGTGGCTTCTCCAAAGGAGCTTGGATGGAATGTGCCACACAGAGCAT 303  
QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGAGCCTGCCGCTGACATCCAGGCTGCCA 360  
DB 304 CACCCAGTGTGACATCTATAGCAACCTTCTGAGCCTGCCGCTGACATCCAGGCTGCCA 363  
QY 361 GGCATATGTGTGACATCCAGTGCATCTCTCCCTGCGCTGCATATCTCTGTGTGG 420  
DB 364 GGCATATGTGTGACATCCAGTGCATCTCTCCCTGCGCTGCATATCTCTGTGTGG 423



421 CATGAGATGACAGTCTTCTGCGAGGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480  
 424 CATGAGATGACAGTCTTCTGCGAGGAAATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483  
 481 TGAAGCTTTTATCCTTGGAGGCGCTCGGAGATTCATCTGTTGCTCGAATCTTCA 540  
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 601 AGAGGCTTTTACTTGGGCAATATTTCTTCTGTTCTCCCTGATAGCTGAAATCATCTT 660  
 604 AGAGGCTTTTACTTGGGCAATATTTCTTCTGTTCTCCCTGATAGCTGAAATCATCTT 663  
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 664 CTGCTTTCTGCTCATCCGAGGAAATGCTCCAACTACTAGATGCTTCAAGGCCCA 723  
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 784 CAATTCCTACAGCTGACAGGCTATGTGTAAAGAACAGGGGCGACAGCTGGGGGCTGGC 843  
 841 TGGGCTGTGAAAGAGTGTGACAGCAGCCCGAGGGGCGACAGGATGAGGAGCACTACCACT 900  
 844 TGGGCTGTGAAAGAGTGTGACAGCAGCCCGAGGGGCGACAGGATGAGGAGCACTACCACT 903  
 901 GATTCGTGACAGAGTGTGCTGAGAGTATGACTGATTTGGCATTTGATGAGCAAG 960  
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 1084 GAAACCCCATTTCCCTTAAGCCAGGACTCAGAGATCCCTTTGCTGCTTGAACCTGGG 1143  
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 1201 TCTCTGAGTGAAGTGTGCTTGAAGTCAATGCTGAGGAGTGGGAAAGAAAGAGATGGC 1260  
 1204 TCTCTGAGTGAAGTGTGCTTGAAGTCAATGCTGAGGAGTGGGAAAGAAAGAGATGGC 1263  
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 1321 TGAAGCTCATCCCACTCTTGTATGATCTCCAGAGTGTGCAAGCTAATTTTGTGATGAA 1380  
 1324 TGAAGCTCATCCCACTCTTGTATGATCTCCAGAGTGTGCAAGCTAATTTTGTGATGAA 1383  
 1381 CTGAAATTAAGATCTCTAGAGTTCAGAGGAAAGAAAGAGATGAGAGTGGAGGA 1440  
 1384 CTGAAATTAAGATCTCTAGAGTTCAGAGGAAAGAAAGAGATGAGAGTGGAGGA 1443  
 1441 CAGGAGGAGAGCTGGAGCATTTAAAAAATA 1472  
 1444 CAGGAGGAGAGCTGGAGCATTTAAAAAATA 1475

RESULT 4  
 US-10-006-867-79  
 ; Sequence 79, Application US/10006867  
 ; Publication No. US20020119130A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerilben, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3230R1C1  
 ; CURRENT APPLICATION NUMBER: US/10/006,867  
 ; CURRENT FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: 60/063435  
 ; PRIOR FILING DATE: 1997-10-29  
 ; PRIOR APPLICATION NUMBER: 60/064215  
 ; PRIOR FILING DATE: 1997-10-29  
 ; PRIOR APPLICATION NUMBER: 60/082797  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/083495  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
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 DB 64 GCTTCAGCCTGAGAGAGAGAGAGCTGGAATGAGGATTAGAGGTTCAGAGAGAGA 123  
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DB 244 GACAGCAGTTGGCTTCTCCAAAGGCTCTGGAATGGAATGTGCAACACAGCAGAGCAT 303
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DB 304 CACCAAGTGTGACATCTATAGCACTTCTGGGCTGCGCGCTGACATCCAGGCTGCCA 363
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QY 421 CATGAGATGCAAGTCTTCTGCGCAGGAATCCGAGCCAAAGACAGATGGCGGTAGCAG 480
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## RESULT 5

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; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 79
; LENGTH: 1475
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US-10-028-072-491

Sequence 491, Application US/10028072

Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
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;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088730  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088741  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090538  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGCCTGGCAGAGAGACTGGAATGAGGATTAGAGTTCAGAGAGAGA 60  
Db 4 AGAAGTCAGCCTGGCAGAGAGACTGGAATGAGGATTAGAGTTCAGAGAGAGA 63  
QY 61 GCTTCAGCCTGGAAGACAGAGGAGCACTCCCTGGAAGCGCTTCTAAGAGGCTTCGCAT 120  
Db 64 GCTTCAGCCTGGAAGACAGAGGAGCACTCCCTGGAAGCGCTTCTAAGAGGCTTCGCAT 123  
QY 121 GGCCTCTTGGGCTTCAACTTGTGGGCTACATCTCAAGGCTTCTGGGGCTTTGGGCAC 180  
Db 124 GGCCTCTTGGGCTTCAACTTGTGGGCTACATCTCAAGGCTTCTGGGGCTTTGGGCAC 183  
QY 181 ACTGGTTGCATGCTGCTCCCGCAGCTGGAAGCAAGTTCTTATGTGGTGCAGCATTTG 240  
Db 184 ACTGGTTGCATGCTGCTCCCGCAGCTGGAAGCAAGTTCTTATGTGGTGCAGCATTTG 243  
QY 241 GACAGCAGTTGGCTTCCAGAGGCGCTGTGATGATGTGCCACACAGCAGAGGCAT 300  
Db 244 GACAGCAGTTGGCTTCCAGAGGCGCTGTGATGATGTGCCACACAGCAGAGGCAT 303  
QY 301 CACCCAGTGTGAATCTATAGCACCCTTGTGGGCTGCCCGCTGAATCTCAGGCTGCCCA 360  
Db 304 CACCCAGTGTGAATCTATAGCACCCTTGTGGGCTGCCCGCTGAATCTCAGGCTGCCCA 363

OY	361	GGCCATGATGGGATCATCCAGTGCATCTCTCCCTGGCTGCATTAATCTCTGTGGTGG	420
Db	364	GGCCATGATGGGATCATCCAGTGCATCTCTCTCCCTGGCTGCATTAATCTCTGTGGTGG	423
OY	421	CATGAGATGCACGTCCTTCTGCGAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAG	480
Db	424	CATGAGATGCACAGTCCTTCTGCGAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAG	483
OY	481	TGGAGTCTTTTTCATCCCTTGGAGGGCTCCTGGGATTTCAATTCTGTGTGCTGGAACTTCA	540
Db	484	TGGAGTCTTTTTCATCCCTTGGAGGGCTCCTGGGATTTCAATTCTGTGTGCTGGAACTTCA	543
OY	541	TGGAGTCCAGGGGACTTCTACTACCACTGGTGGCTGACAGATGAATTTGAGATTGG	600
Db	544	TGGAGTCCAGGGGACTTCTACTACCACTGGTGGCTGACAGATGAATTTGAGATTGG	603
OY	601	AGAGGCTCTTACTTGGGCAATTATTTCTCCCTGTCTTCCCTGATAGCTGAAATCATCT	660
Db	604	AGAGGCTCTTACTTGGGCAATTATTTCTCCCTGTCTTCCCTGATAGCTGAAATCATCT	663
OY	661	CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCCACTTCTAGATGCTTACCAAGCCCA	720
Db	664	CTGCTTTTCTGCTCATCTCCAGAGAAATGCTTCCACTTCTAGATGCTTACCAAGCCCA	723
OY	721	ACCTCTTGCCACAAGAGGCTCCCAAGGCGTGGTCAACCTCCCAAGTCAAGAGAGTT	780
Db	724	ACCTCTTGCCACAAGAGGCTCCCAAGGCGTGGTCAACCTCCCAAGTCAAGAGAGTT	783
OY	781	CAATTCTCTACAGCTGTACAGAGGTATGTGTGAAGAAACAGAGGGCCAGAGCTGGGGGTGGC	840
Db	784	CAATTCTCTACAGCTGTACAGAGGTATGTGTGAAGAAACAGAGGGCCAGAGTGAAGGATCTGCACT	843
OY	841	TGGGTCTGTGAAAAACAGTGGACAGACCCCGAGGGCCACAGGTGAAGGATCTTACACT	900
Db	844	TGGGTCTGTGAAAAACAGTGGACAGACCCCGAGGGCCACAGGTGAAGGATCTTACACT	903
OY	901	GGATGTGTGCAAGAAAGTGTGCTGTGAGATGACGTACTTTGGCCATTTGGATGAGCAAG	960
Db	904	GGATGTGTGCAAGAAAGTGTGCTGTGAGATGACGTACTTTGGCCATTTGGATGAGCAAG	963
OY	961	GCAGAAATGGGGGCTAGTGTAAACAGATGCAGAGTTGAATTTGCCAAGATGCTCGCCATGC	1020
Db	964	GCAGAAATGGGGGCTAGTGTAAACAGATGCAGAGTTGAATTTGCCAAGATGCTCGCCATGC	1022
OY	1021	CAGCCTTCTGTCTTCTTACCTGTGCTGCTGCCCTGACCTTAAGTCCCAACCTCACTT	1080
Db	1024	CAGCCTTCTGTCTTCTTACCTGTGCTGCTGCCCTTAAGTCCCAACCTCACTT	1083
OY	1081	GAAACCCCAATTCCTTAAGCCAGAGACTCAGAGAAATCCCTTGGCTCTGTGTTTACTGGG	1144
Db	1084	GAAACCCCAATTCCTTAAGCCAGAGACTCAGAGAAATCCCTTGGCTCTGTGTTTACTGGG	1147
OY	1141	ACTCATCCCCCAAAACCACTAATGACATCCCACTGACCTCCTGTGATCAAAAGCCC	1200
Db	1144	ACTCATCCCCCAAAACCACTAATGACATCCCACTGACCTCCTGTGATCAAAAGCCC	1203
OY	1201	TCTCTCTGAGCTGAGGTGGCTCTTAAGCTTATGCTGTGGGATGGAGAGGAAGCAGTGGC	1260
Db	1204	TCTCTCTGAGCTGAGGTGGCTCTTAAGCTTATGCTGTGGGATGGAGAGGAAGCAGTGGC	1263
OY	1261	TTTTGTGGGCAATGCTCTTAACCTACTTCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC	1322
Db	1264	TTTTGTGGGCAATGCTCTTAACCTACTTCTCAAGCTTCCCTCAAAAGAACTGATTGGCCC	1325
OY	1321	TGGAACCTCCAACTCCACTTGTATGATCCACAGTGCAGAGCTAAATTTGTGATGAA	1380
Db	1324	TGGAACCTCCAACTCCACTTGTATGATCCACAGTGCAGAGCTAAATTTGTGATGAA	1383
OY	1381	CTGAAATTAACCAATCTCTACGGTATCCAGGGAAACAGAAAGCAGATGCAAGATGGGAGGA	1440
Db	1384	CTGAAATTAACCAATCTCTACGGTATCCAGGGAAACAGAAAGCAGATGCAAGATGGGAGGA	1443
OY	1441	CAGGAAGCAGCTGGGACATTTAAAAAATA 1472	

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RESULT 8
US-10-063-616-79
; Sequence 79, Application US/1006316
; Publication No. US2003013855A1
GENERAL INFORMATION:
; APPLICANT: Ealon, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063.616
PRIOR FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 79
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-79

Query Match      53.7%; Score 1472; DB 14; Length 1475;
Best Local Similarity 100.0%; Pident. No. 0;
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DB      1444 CAGGAGGACGCTGGGACATTTAAAAAATA 1475

1  AGAAGTCAGCTCGGACAGAGAGACTCTGAATAGAGGATTAGAGGTGTTCAAGAGACAGA 60
4  AGAAGTCAGCTCGGACAGAGAGACTCTGAATAGAGGATTAGAGGTGTTCAAGAGACAGA 63
61  GCTTCAGCTTGGAAGACAAGGAGAGAGCTCCCTGAAGACGCTTCTACTGAGAGGCTTGCAT 120
64  GCTTCAGCTTGGAAGACAAGGAGAGAGCTCCCTGAAGACGCTTCTACTGAGAGGCTTGCAT 123
121  GGCCTCTCTTGGCTCCCACTTTGGGCTAATCCTAGGCTTCTGGGGCTTTTGGGCAC 180
124  GGCCTCTCTTGGCTCCCACTTTGGGCTAATCCTAGGCTTCTGGGGCTTTTGGGCAC 183
181  ACTGGTTGCGATGCTGCTCCGACGTGGGAAAACAAGTCTTATGCGGGTGCAGCATTTG 240
184  ACTGGTTGCGATGCTGCTCCGACGTGGGAAAACAAGTCTTATGCGGGTGCAGCATTTG 243
241  GACAGCAGTTGGCTTCTCCAAAGGGCTCTGATGGATGTGCCACACACAGACAGGAGAT 300
244  GACAGCAGTTGGCTTCTCCAAAGGGCTCTGATGGATGTGCCACACACAGACAGGAGAT 303
301  CACCCAGTGTGACATCTATAGACCCCTTCTGGGCTCTGCCGCTGACATCCAGGCTGCCA 360
304  CACCCAGTGTGACATCTATAGACCCCTTCTGGGCTCTGCCGCTGACATCCAGGCTGCCA 363
361  GGCATATATGGTATGATCAGATGCAATCTCCCTCGGCTGCGATTAATCTCTGTGGTGGG 420
364  GGCATATATGGTATGATCAGATGCAATCTCCCTCGGCTGCGATTAATCTCTGTGGTGGG 423
421  CATGAGATGACAGATCTTCTGCGACAGAAATCCCGAGCCAAAGACAGAGTGGCGGTAGAG 480
424  CATGAGATGACAGATCTTCTGCGACAGAAATCCCGAGCCAAAGACAGAGTGGCGGTAGAG 483
481  TGGAGTCTTTTCAATCCTTGGAGGCTCTCGGATTCATTCCTGTGCTTGGATCTTCA 540
484  TGGAGTCTTTTCAATCCTTGGAGGCTCTCGGATTCATTCCTGTGCTTGGATCTTCA 543
541  TGGAGTCTTACGGGACTTCTACTACCACTGGTGTGCTGACAGCATGAATTTGAGATTGG 600

```





QY 661 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 720  
DB 664 CTGCTTTCTGCTCATCCAGAGAAATCGCTCCAACTACTAGATGCTTACCAAGCCCA 723  
QY 721 ACCCTTGGCCAGAGAGCTCTCCAGAGAGCTCTCCAACTACTAGATGCTTACCAAG 780  
DB 724 ACCCTTGGCCAGAGAGCTCTCCAGAGAGCTCTCCAACTACTAGATGCTTACCAAG 783  
QY 781 CAATTCTAGAGCTGACAGAGGATATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
DB 784 CAATTCTAGAGCTGACAGAGGATATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 843  
QY 841 TGGGCTGTGAG 900  
DB 844 TGGGCTGTGAG 903  
QY 901 GGAATCGTCAAG 960  
DB 904 GGAATCGTCAAG 963  
QY 961 GCAAGAAATGGGGGCTAGATGTAACAGATGCAAGTGAATGCAAGAGAGAGAGAGAG 1020  
DB 964 GCAAGAAATGGGGGCTAGATGTAACAGATGCAAGTGAATGCAAGAGAGAGAGAGAG 1023  
QY 1021 CAGCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCCAACTCACTT 1080  
DB 1024 CAGCTTTCTGTTTCTCTCACTTGTGCTGCTCCCTGCTTAACTGCTCCAACTCACTT 1083  
QY 1081 GAAACCCCATTTCCCTTAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
DB 1084 GAAACCCCATTTCCCTTAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143  
QY 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGAGTGAACCTCTGTATCAAAAGACC 1200  
DB 1144 ACTTCATCCCAAAACCACTAATCAATCCCACTGAGTGAACCTCTGTATCAAAAGACC 1203  
QY 1201 TCTCTGCTGAGTGGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGAGAGAG 1260  
DB 1204 TCTCTGCTGAGTGGTGGCTCTTAAGCTCATTTGCTGGAGATGGAGAGAGAGAGAG 1263  
QY 1261 TTTTGTGGGAGTGGCTTAACCTTCTCAAGTCTCCCTCAAAAGAACTGATTTGAGCC 1320  
DB 1264 TTTTGTGGGAGTGGCTTAACCTTCTCAAGTCTCCCTCAAAAGAACTGATTTGAGCC 1323  
QY 1321 TGGAACTCCATCCCACTCTTGTATGACTCCAGAGTCCAGAGTCAATTTGTGATGAA 1380  
DB 1324 TGGAACTCCATCCCACTCTTGTATGACTCCAGAGTCCAGAGTCAATTTGTGATGAA 1383  
QY 1381 CTGAATTAACCACTCTTACGATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
DB 1384 CTGAATTAACCACTCTTACGATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
QY 1441 CAGGAGGAGGCTGGGAGCAATTTAAAAATA 1472  
DB 1444 CAGGAGGAGGCTGGGAGCAATTTAAAAATA 1475

RESULT 10  
US-10-063-569-79

Sequence 79, Application US/10063569  
Publication No. US20030018168A1  
GENERAL INFORMATION:  
APPLICANT: Bacon, Dan L.  
APPLICANT: Pivaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,569  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 79  
LENGTH: 1475  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-569-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTCAGGCTGGCAGAGAGAGTCTGAAATGAGGAGATTAAGAGTTCAGAGAGAGAG 60  
DB 4 AGAAGTCAGGCTGGCAGAGAGAGTCTGAAATGAGGAGATTAAGAGTTCAGAGAGAGAG 63  
QY 61 GCTTCAGGCTGAAAG 120  
DB 64 GCTTCAGGCTGAAAG 123  
QY 121 GGCCTCTTGGGCTCCAACTTGTGGGCTAATCTTAAAGCCTTCTGGGCTTTTGGGCA 180  
DB 124 GGCCTCTTGGGCTCCAACTTGTGGGCTAATCTTAAAGCCTTCTGGGCTTTTGGGCA 183  
QY 181 ACTGTTGACATGCTGCTCCGAGCTGAGAAACAAATTTCTTATGTGCGTGCAGAGATGT 240  
DB 184 ACTGTTGACATGCTGCTCCGAGCTGAGAAACAAATTTCTTATGTGCGTGCAGAGATGT 243  
QY 241 GACAGAGATGGCTTCTCAAGAGGCTCTGATGAGATGTGCCACACAGAGAGAGAGAT 300  
DB 244 GACAGAGATGGCTTCTCAAGAGGCTCTGATGAGATGTGCCACACAGAGAGAGAGAT 303  
QY 301 CACCAAGTGAATATCTAATAGACACCTTGTGGGCTGCCGCTGAGATCAAGGCTGCCA 360  
DB 304 CACCAAGTGAATATCTAATAGACACCTTGTGGGCTGCCGCTGAGATCAAGGCTGCCA 363  
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423  
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
QY 481 TGAAGTCTTTTCAATCTTGAAGGCTCTGAGATTTCAATCTTGAAGTCTTTTCA 540  
DB 484 TGAAGTCTTTTCAATCTTGAAGGCTCTGAGATTTCAATCTTGAAGTCTTTTCA 543  
QY 541 TGGAGTCTTACGAGAGCTTCACTCACAGTGTGCTGACAGAGATTAATTTGAGATTG 600  
DB 544 TGGAGTCTTACGAGAGCTTCACTCACAGTGTGCTGACAGAGATTAATTTGAGATTG 603  
QY 601 AGAGGCTCTTACTTGGGAGATTAATTTCTTCTGTTCTCTCTGATAGCTGAAATCACT 660  
DB 604 AGAGGCTCTTACTTGGGAGATTAATTTCTTCTGTTCTCTCTGATAGCTGAAATCACT 663  
QY 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCCAACTACTAGATGCTTACCAAGCCCA 720  
DB 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTTCCAACTACTAGATGCTTACCAAGCCCA 723  
QY 721 ACCCTTGGCCAGAGAGCTCTCCAGAGAGCTCTCCAACTACTAGATGCTTACCAAGAG 780  
DB 724 ACCCTTGGCCAGAGAGCTCTCCAGAGAGCTCTCCAACTACTAGATGCTTACCAAGAG 783  
QY 781 CAATTCTAGAGCTGACAGAGGATATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
DB 784 CAATTCTAGAGCTGACAGAGGATATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 843  
QY 841 TGGGCTGTGAG 900

Db 844 TGGGCTGTGTAAGAAACAGTGAACAGACCCCGAGGGGACAGGTGAGGGAACATCACT 903  
Qy 901 GGATCGGTGAGAAAGGCTGTGAGGATGAGATGATCTTTGGCCATTGATGAGCAAG 960  
Db 904 GGATCGGTGAGAAAGGCTGTGAGGATGAGATGATCTTTGGCCATTGATGAGCAAG 963  
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGATGAGATGAGATGAGATGAGATGAGATGAG 1020  
Db 964 GCAGAAATGGGGGCTAGTGTAAACAGATGAGATGAGATGAGATGAGATGAGATGAG 1023  
Qy 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db 1024 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
Qy 1081 GAAACCCCATCTCTTAAGCAGGATCAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCT 1140  
Db 1084 GAAACCCCATCTCTTAAGCAGGATCAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCT 1143  
Qy 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGATGATCCCTGCTGCTGCTGCTGCT 1200  
Db 1144 ACTTCATCCCAAAACCACTAATCAATCCCACTGATGATCCCTGCTGCTGCTGCTGCT 1203  
Qy 1201 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
Db 1204 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
Qy 1261 TTTTGTGGGCAATGCTTAACTTCTTCAAGCTTCCCTCAAGAACTGATTTGCTGCT 1320  
Db 1264 TTTTGTGGGCAATGCTTAACTTCTTCAAGCTTCCCTCAAGAACTGATTTGCTGCT 1323  
Qy 1321 TGGAACTCCCATCCCACTCTTGTATGATCTCAAGTGTCCAGACTAATTTGCTGCT 1380  
Db 1324 TGGAACTCCCATCCCACTCTTGTATGATCTCAAGTGTCCAGACTAATTTGCTGCT 1383  
Qy 1381 CTGAATTAACCACTCTTGTATGATCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Db 1384 CTGAATTAACCACTCTTGTATGATCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAG 1443  
Qy 1441 CAGGAAGGAGGCTGAGCAATTTAAAAATA 1472  
Db 1444 CAGGAAGGAGGCTGAGCAATTTAAAAATA 1475

## RESULT 11

US-10-063-513-79  
; Sequence 79, Application US/10063513  
; Publication No. US20030018172A1  
; GENERAL INFORMATION:  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Rilveroff, Ellen  
; APPLICANT: Gerriksen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P323081C1  
; CURRENT APPLICATION NUMBER: US/10/063, 513  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 79  
; LENGTH: 1475  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-513-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAAGCTGGCAGAGAGACTGTGAATGAGGATTTAGAGTGTTCAGAGAGAGA 60  
Db 4 AGAAGTCAAGCTGGCAGAGAGACTGTGAATGAGGATTTAGAGTGTTCAGAGAGAGA 63  
Qy 61 GCTTCAGCTGAAAGACAGAGGAGCACTCCCTGTAAGACGCTTCTAATGAGAGGCTGCT 120  
Db 64 GCTTCAGCTGAAAGACAGAGGAGCACTCCCTGTAAGACGCTTCTAATGAGAGGCTGCT 123  
Qy 121 GGGCTCTTGGGCTCAACTGTGGGCTAATCCTAAGGCTTCTGGGGCTTTTGGGCA 180  
Db 124 GGGCTCTTGGGCTCAACTGTGGGCTAATCCTAAGGCTTCTGGGGCTTTTGGGCA 183  
Qy 181 ACTGTTGCAATCTGCTCCCACTGAGAAACAAAGTTCTTATGTGTGCTGCAATGCT 240  
Db 184 ACTGTTGCAATCTGCTCCCACTGAGAAACAAAGTTCTTATGTGTGCTGCAATGCT 243  
Qy 241 GACAGAGTTGGCTTCCAGAGGCTCTGAGATGAAATGTGCCACACAGCAGGCAAT 300  
Db 244 GACAGAGTTGGCTTCCAGAGGCTCTGAGATGAAATGTGCCACACAGCAGGCAAT 303  
Qy 301 CACCAAGTGAATCTAATAGCAACCTTGGGCTGCGCGCTGATCCAGATCCAGGCTGCCA 360  
Db 304 CACCAAGTGAATCTAATAGCAACCTTGGGCTGCGCGCTGATCCAGATCCAGGCTGCCA 363  
Qy 361 GGCATGATGATGACATCCAGTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 364 GGCATGATGATGACATCCAGTCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423  
Qy 421 CATGAGATGACAGTCTTCCAGAGATCCGAGCCAAAGACAGATGGCGGTAGCAG 480  
Db 424 CATGAGATGACAGTCTTCCAGAGATCCGAGCCAAAGACAGATGGCGGTAGCAG 483  
Qy 481 TGGAGTCTTTTCACTCTTGAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 484 TGGAGTCTTTTCACTCTTGAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543  
Qy 541 TGGAGTCTTCAAGGAGCTTCTAATCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 544 TGGAGTCTTCAAGGAGCTTCTAATCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 603  
Qy 601 AGAGGCTCTTCTTCTGAGCAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 604 AGAGGCTCTTCTTCTGAGCAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663  
Qy 661 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGGCCA 720  
Db 664 CTGCTTTCTGCTCATCCAGAGAAATGCTCCAACTAATAGATGCTTCAAGGCCA 723  
Qy 721 ACCCTTGCAGAGAGGCTCTCAAGGCTGCTCAACCTCCCAAGTCAAGAGTGA 780  
Db 724 ACCCTTGCAGAGAGGCTCTCAAGGCTGCTCAACCTCCCAAGTCAAGAGTGA 783  
Qy 781 CAATTCCTAAGCCTGACAGGATATGTGAAGAACCAAGGAGCCAGAGCTGAGGAGTGGC 840  
Db 784 CAATTCCTAAGCCTGACAGGATATGTGAAGAACCAAGGAGCCAGAGCTGAGGAGTGGC 843  
Qy 841 TGGGCTGTGTAAGAAACAGTGAACAGACCCCGAGGGCCACAGGTGAGGACATTAACCT 900  
Db 844 TGGGCTGTGTAAGAAACAGTGAACAGACCCCGAGGGCCACAGGTGAGGACATTAACCT 903  
Qy 901 GGATCGGTGAGAAAGGCTGTGAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 960  
Db 904 GGATCGGTGAGAAAGGCTGTGAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 963  
Qy 961 GCAGAAATGGGGGCTAGTGTAAACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1020  
Db 964 GCAGAAATGGGGGCTAGTGTAAACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1023  
Qy 1021 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db 1024 CAGCCTTTCTGTTTCTCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083

QY 1081 GAAACCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCTGTGTTACTGGG 1140  
 DB 1084 GAAACCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGGCTGTGTTACTGGG 1143  
 QY 1141 ACTCCATCCCAAAACCATTAATCAATCCCACTGAACCCCTGTGTATCAAAAGCCC 1200  
 DB 1144 ACTCCATCCCAAAACCATTAATCAATCCCACTGAACCCCTGTGTATCAAAAGCCC 1203  
 QY 1201 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGGATGGAGAGAGAGAGAGG 1260  
 DB 1204 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGGATGGAGAGAGAGAGG 1263  
 QY 1261 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTCCCTCAAGAACTGAATGGCCC 1320  
 DB 1264 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTCCCTCAAGAACTGAATGGCCC 1323  
 QY 1321 TGAACCTCATCCACTCTTTGTTATGATCCACAGTCCAGCTAACTTGTGCAATGA 1380  
 DB 1324 TGAACCTCATCCACTCTTTGTTATGATCCACAGTCCAGCTAACTTGTGCAATGA 1383  
 QY 1381 CTGAATTAATAACATCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 1440  
 DB 1384 CTGAATTAATAACATCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 1443  
 QY 1441 CAGGAAGGCGCTGGGACATTTAAAAATA 1472  
 DB 1444 CAGGAAGGCGCTGGGACATTTAAAAATA 1475

RESULT 12

US-10-063-515-79  
 / Sequence 79, Application US/10063515  
 / Publication No. US2003018173A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Ealon, Dan L.  
 / APPLICANT: Geriltsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, Christopher J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Metanabe, Colin K.  
 / APPLICANT: Wood, William I.  
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 / FILE REFERENCE: P3230R1C1  
 / CURRENT APPLICATION NUMBER: US/10/063,515  
 / PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 / NUMBER OF SEQ ID NOS: 170  
 / SEQ ID NO 79  
 / LENGTH: 1475  
 / TYPE: DNA  
 / ORGANISM: Homo Sapien  
 / US-10-063-515-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTAGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGTGTTCAGAGAGAGAG 60  
 DB 4 AGAAGTAGCTGGCAGAGAGACTCTGAATAGAGGATTAGAGTGTTCAGAGAGAGAG 63  
 QY 61 GCTTCAGCTGAAG 120  
 DB 64 GCTTCAGCTGAAG 123  
 QY 121 GGGCTCTTGGCTCTCAACCTTGTGGCTACATCTCAAGGCTTCTGGGGCTTTTGGGAC 180  
 DB 124 GGGCTCTTGGCTCTCAACCTTGTGGCTACATCTCAAGGCTTCTGGGGCTTTTGGGAC 183  
 QY 181 ACTGTGGCATGTGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

DB 184 ACTGTGGCATGTGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243  
 QY 241 GACAGAGTGGCTTCTCCAG 300  
 DB 244 GACAGAGTGGCTTCTCCAG 303  
 QY 301 CACCAAGTGAATATTAATAGCAACCTTGGGCTGCGCGCTGACATCAAGCTGCGCA 360  
 DB 304 CACCAAGTGAATATTAATAGCAACCTTGGGCTGCGCGCTGACATCAAGCTGCGCA 363  
 QY 361 GGGCATGATGATGATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 DB 364 GGGCATGATGATGATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423  
 QY 421 CATGATGATCAAGTCTTTCAG 480  
 DB 424 CATGATGATCAAGTCTTTCAG 483  
 QY 481 TGAAGTCTTTTCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 DB 484 TGAAGTCTTTTCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543  
 QY 541 TGGAGTCTTAAGGAG 600  
 DB 544 TGGAGTCTTAAGGAG 603  
 QY 601 AGAGGCTCTTAAGTGGGAG 660  
 DB 604 AGAGGCTCTTAAGTGGGAG 663  
 QY 661 CTGCTTTTCTGCTGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 DB 664 CTGCTTTTCTGCTGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723  
 QY 721 ACCTCTTGCAAG 780  
 DB 724 ACCTCTTGCAAG 783  
 QY 781 CAATTCCTACAGCTGACAG 840  
 DB 784 CAATTCCTACAGCTGACAG 843  
 QY 841 TGGGTCTGAAAAACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
 DB 844 TGGGTCTGAAAAACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903  
 QY 901 GATTCGTGCAAG 960  
 DB 904 GATTCGTGCAAG 963  
 QY 961 GCAGAAATGGGGCTAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
 DB 964 GCAGAAATGGGGCTAGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023  
 QY 1021 CAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTCAAGTCCCAAGCTCAACTT 1080  
 DB 1024 CAGCTTTCTGTTTCTCACTTGTGCTGCTCCCTGCTCAAGTCCCAAGCTCAACTT 1083  
 QY 1081 GAAACCCATTCCTTAAGCAG 1140  
 DB 1084 GAAACCCATTCCTTAAGCAG 1143  
 QY 1141 ACTCCATCCCAAAACCATTAATCAATCCCACTGAACCCCTGTGTATCAAAAGCCC 1200  
 DB 1144 ACTCCATCCCAAAACCATTAATCAATCCCACTGAACCCCTGTGTATCAAAAGCCC 1203  
 QY 1201 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGGATGGAGAGAGAGAGAGG 1260  
 DB 1204 TCTCTGAGTGAAGTGGCTCTTAAGCTCATTTGCTGGGATGGAGAGAGAGAGAGG 1263  
 QY 1261 TTTTGTGGGATGCTCTTAACCTTAAGCTCTCAAGCTCCCTCAAGAACTGAATGGCCC 1320

Db 1264 TTTTGGGCGATTCCTTAACCTTCTCAAGCTTCCCTCCAAAGAAATGATTTGGCCC 1323  
 Qy 1321 TGGAACTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCATGAA 1380  
 Db 1324 TGGAACTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCATGAA 1383  
 Qy 1381 CTGAATTAACCAATCTTACGCTATCCAGGAAACAGAAAGAGATGAGATGGAGGA 1440  
 Db 1384 CTGAATTAACCAATCTTACGCTATCCAGGAAACAGAAAGAGATGAGATGGAGGA 1443  
 Qy 1441 CAGGAAGGAGCTGGGAGCATTTAAAAATA 1472  
 Db 1444 CAGGAAGGAGCTGGGAGCATTTAAAAATA 1475

RESULT 13

US-10-063-512-79  
 ; Sequence 79, Application US/10063512  
 ; Publication No. US200300183A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3230R1C1  
 ; CURRENT APPLICATION NUMBER: US/10/063.512  
 ; PRIORITY FILING DATE: 2002-05-01  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SEQ ID NO 79  
 ; LENGTH: 1475  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-063-512-79

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAAGTCAGCTTGGCAGAGAGACTCTGAATGAGGATTAAGGTCTTCAAGAGCAAGA 60  
 Db 4 AGAAGTCAGCTTGGCAGAGAGACTCTGAATGAGGATTAAGGTCTTCAAGAGCAAGA 63  
 Qy 61 GCTTCAGCTGGAAGCAAGGAGAGAGCTCCAGAGAGCTTCTAAGAGTCTGCAT 120  
 Db 64 GCTTCAGCTGGAAGCAAGGAGAGAGCTCCAGAGAGCTTCTAAGAGTCTGCAT 123  
 Qy 121 GGCCTCTCTTGGCTCCCAACTTGTGGCTACATCTTGAAGCTTGTGGGCTTTTGGGAC 180  
 Db 124 GGCCTCTCTTGGCTCCCAACTTGTGGCTACATCTTGAAGCTTGTGGGCTTTTGGGAC 183  
 Qy 181 ACTGTTGCGCATGCTGCTCCCAAGCTGGAAGCAAGTCTTATGTGGTGCAGCATTTGT 240  
 Db 184 ACTGTTGCGCATGCTGCTCCCAAGCTGGAAGCAAGTCTTATGTGGTGCAGCATTTGT 243  
 Qy 241 GACGAGAGTTGGCTTCTCCAAAGGCTCTGAGTGAATGTGCAACAGCAAGGAGAT 300  
 Db 244 GACGAGAGTTGGCTTCTCCAAAGGCTCTGAGTGAATGTGCAACAGCAAGGAGAT 303  
 Qy 301 CACCAAGTGTGACATCTTAAGCAACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 360  
 Db 304 CACCAAGTGTGACATCTTAAGCAACCTTCTGGGCTGCGCTGACATCCAGGCTGCCA 363  
 Qy 361 GGCATATGATGATGATCAGTGCATCTCTCCCTGGGCTGCAATTAATCTTGTGTGG 420  
 Db 364 GGCATATGATGATGATCAGTGCATCTCTCCCTGGGCTGCAATTAATCTTGTGTGG 423

Qy 421 CATGAGATGACAGTCTTCTGCGAGAGATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480  
 Db 424 CATGAGATGACAGTCTTCTGCGAGAGATCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483  
 Qy 481 TGAAGTCTTTTCACTCTTGAAGGCTCTCTGGATTAATCTCTGTCTCTGGAATCTTCA 540  
 Db 484 TGAAGTCTTTTCACTCTTGAAGGCTCTCTGGATTAATCTCTGTCTCTGGAATCTTCA 543  
 Qy 541 TGGATCTCTACGGAGCTTCTACTACACAGTGTGCTGAGAGATGAATTTTGAATGG 600  
 Db 544 TGGATCTCTACGGAGCTTCTACTACACAGTGTGCTGAGAGATGAATTTTGAATGG 603  
 Qy 601 AGAGGCTCTTACTTGGGCAATTAATTTCTCTCTGTTCTCTCTGATGCTGAATCATCT 660  
 Db 604 AGAGGCTCTTACTTGGGCAATTAATTTCTCTCTGTTCTCTCTGATGCTGAATCATCT 663  
 Qy 661 CTGCTTTTCTGCTCATCCAGAGAAATGCTCTCAACTTACAGATGCTTACCAAGCCCA 720  
 Db 664 CTGCTTTTCTGCTCATCCAGAGAAATGCTCTCAACTTACAGATGCTTACCAAGCCCA 723  
 Qy 721 ACCTTGGCAAGAGAGCTCTCAAGGCTGCTGCAACCTCCAAAGTCAAGTGAAT 780  
 Db 724 ACCTTGGCAAGAGAGCTCTCAAGGCTGCTGCAACCTCCAAAGTCAAGTGAAT 783  
 Qy 781 CAATTCTACAGCTGACAGGATATGTGAAGAACAGAGGCTGAGGCTGAGGCTGAGC 840  
 Db 784 CAATTCTACAGCTGACAGGATATGTGAAGAACAGAGGCTGAGGCTGAGGCTGAGC 843  
 Qy 841 TGGCTCTGTAAGAAACAGTGAACAGACCCCGAGGCTCAAGTGAAGACATCACT 900  
 Db 844 TGGCTCTGTAAGAAACAGTGAACAGACCCCGAGGCTCAAGTGAAGACATCACT 903  
 Qy 901 GATGCTGTAAGAAAGGCTGTAAGATGATGATGATGATGATGATGATGATGATGATG 960  
 Db 904 GATGCTGTAAGAAAGGCTGTAAGATGATGATGATGATGATGATGATGATGATGATG 963  
 Qy 961 GCAAGAAATGGGCTGATGTAAGAGATGAGATGATGATGATGATGATGATGATGATG 1020  
 Db 964 GCAAGAAATGGGCTGATGTAAGAGATGAGATGATGATGATGATGATGATGATGATG 1023  
 Qy 1021 CAGCTTCTGTTTCTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 Db 1024 CAGCTTCTGTTTCTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1083  
 Qy 1081 GAAACCCATTTCTTAAAGCAGAGATCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 Db 1084 GAAACCCATTTCTTAAAGCAGAGATCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1143  
 Qy 1141 ACTTCATCCCAAAACCACTAATCAATCCCACTGACCTGCTGCTGCTGCTGCTGCTG 1200  
 Db 1144 ACTTCATCCCAAAACCACTAATCAATCCCACTGACCTGCTGCTGCTGCTGCTGCTG 1203  
 Qy 1201 TCTCTGCTGAGTGTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 Db 1204 TCTCTGCTGAGTGTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263  
 Qy 1261 TTTTGTGGCATGCTCTTAACTTCTCAAGCTTCTCTCAAGAAATGATTTGGCCC 1320  
 Db 1264 TTTTGTGGCATGCTCTTAACTTCTCAAGCTTCTCTCAAGAAATGATTTGGCCC 1323  
 Qy 1321 TGGAACTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCATGAA 1380  
 Db 1324 TGGAACTCCATCCCACTCTTGTATGATCCAGAGTCCAGACTAATTTGTGCATGAA 1383  
 Qy 1381 CTGAATTAACCAATCTTACGCTATCCAGGAAACAGAAAGAGATGAGATGGAGGA 1440  
 Db 1384 CTGAATTAACCAATCTTACGCTATCCAGGAAACAGAAAGAGATGAGATGGAGGA 1443  
 Qy 1441 CAGGAAGGAGCTGGGAGCATTTAAAAATA 1472  
 Db 1444 CAGGAAGGAGCTGGGAGCATTTAAAAATA 1475

RESULT 14  
US-10-121-049-491  
; Sequence 491, Application US/10121049  
; Publication No. US2003002239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P330R1C17  
; CURRENT APPLICATION NUMBER: US/10/121,049  
; PRIORITY FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 491  
; LENGTH: 1475  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-121-049-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGACTCTGAATAGAGGATAGAGGTTCAGAGGACAGA 60  
DB 4 AGAAGTACGCTGGCAGAGACTCTGAATAGAGGATAGAGGTTCAGAGGACAGA 63  
QY 61 GCTTCAAGCTGAGAGAGAGGAGAGTCCCTGAGAGAGCTTCTACTGAGAGTCTGCCAT 120  
DB 64 GCTTCAAGCTGAGAGAGAGGAGAGTCCCTGAGAGAGCTTCTACTGAGAGTCTGCCAT 123  
QY 121 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTTCTGGGGCTTTTGGGCAC 180  
DB 124 GGCCTCTCTTGGCCTCCAACTTGTGGGCTACATCTAAGGCTTCTGGGGCTTTTGGGCAC 183  
QY 181 ACTGTTGGCCATGCTGCTCCCGAGCTGAAAACAAAGTTCTTATGTCGGTGCAGCATTTGT 240  
DB 184 ACTGTTGGCCATGCTGCTCCCGAGCTGAAAACAAAGTTCTTATGTCGGTGCAGCATTTGT 243  
QY 241 GACAGCAGTTGGCTTCTCCAGAGGCTCTGGATGGAATGTGCCACACAGACAGAGCAT 300  
DB 244 GACAGCAGTTGGCTTCTCCAGAGGCTCTGGATGGAATGTGCCACACAGAGCAT 303  
QY 301 CACCAAGTGTGACATCTATAGCACTTCTGGGGCTGCGCGTGACATCCAGGCTGGCCA 360  
DB 304 CACCAAGTGTGACATCTATAGCACTTCTGGGGCTGCGCGTGACATCCAGGCTGGCCA 363  
QY 361 GGCCTATATGTTGACATCCAGTCAATCTCTCCCTGGCGCTGCAATTTCTGTGGTGGG 420  
DB 364 GGCCTATATGTTGACATCCAGTCAATCTCTCCCTGGCGCTGCAATTTCTGTGGTGGG 423  
QY 421 CATGAGATGACAGTCTTCTGCGCAGAGATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 480  
DB 424 CATGAGATGACAGTCTTCTGCGCAGAGATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG 483  
QY 481 TGAGATCTTTTTCATCTCTGGAGGCTCTCGGATTCATTCCTGTTGCTGGAATCTTCA 540

DB 484 TGAGATCTTTTTCATCTCTGGAGGCTCTCGGATTCATTCCTGTTGCTGGAATCTTCA 543  
QY 541 TGGGATCTACGGGACTTCTACTCACCAGTGTGCTGACAGCANTGAATTTGAGATTGG 600  
DB 544 TGGGATCTACGGGACTTCTACTCACCAGTGTGCTGACAGCANTGAATTTGAGATTGG 603  
QY 601 AGAGGCTCTTACTTGGGCAATTTTCTCCCTGTTCTCCCTGATATGCTGGAATCTCT 660  
DB 604 AGAGGCTCTTACTTGGGCAATTTTCTCCCTGTTCTCCCTGATATGCTGGAATCTCT 663  
QY 661 CTGCTTTCTCTGCTACATCCAGAGAAATGCTCCAACTACTACGATGCTTACCAAGCCA 720  
DB 664 CTGCTTTCTCTGCTACATCCAGAGAAATGCTCCAACTACTACGATGCTTACCAAGCCA 723  
QY 721 ACCTTTGCGACAGAGAGCTCTCCAGAGGCTGTGTCACTCCCAAGTCAAGTAGATT 780  
DB 724 ACCTTTGCGACAGAGAGCTCTCCAGAGGCTGTGTCACTCCCAAGTCAAGTAGATT 783  
QY 781 CAATTCCTACAGCTTGAACAGGATATGTGAGAAACCAAGGAGCAGAGCTGGGGGGTGGC 840  
DB 784 CAATTCCTACAGCTTGAACAGGATATGTGAGAAACCAAGGAGCAGAGCTGGGGGGTGGC 843  
QY 841 TGGGCTCTGGAATAACAGTGAACAGACACCCGAGGGCCACAGGTGAGGACACTACACT 900  
DB 844 TGGGCTCTGGAATAACAGTGAACAGACACCCGAGGGCCACAGGTGAGGACACTACACT 903  
QY 901 GGATCGTGTGAGAGGTGTGCTGAGATAGACTGATCTTTGGCATTGATTTAGCAAG 960  
DB 904 GGATCGTGTGAGAGGTGTGCTGAGATAGACTGATCTTTGGCATTGATTTAGCAAG 963  
QY 961 GCAGAAATGGGGGCTAGTGAACAGCATGACAGTGAATTTGCCAAGAGTCTGGCATTC 1020  
DB 964 GCAGAAATGGGGGCTAGTGAACAGCATGACAGTGAATTTGCCAAGAGTCTGGCATTC 1023  
QY 1021 CAGCCTTCTGTTTCTCTCACTGCTGCTCCCTGCGCTTAAAGTCCCAACCTCACTT 1080  
DB 1024 CAGCCTTCTGTTTCTCTCACTGCTGCTCCCTGCGCTTAAAGTCCCAACCTCACTT 1083  
QY 1081 GAAACCCCATTCCTTTAAGCAGAGACTCAGAGAGTCCCTTGGCTCTGATTTA 1140  
DB 1084 GAAACCCCATTCCTTTAAGCAGAGACTCAGAGAGTCCCTTGGCTCTGATTTA 1143  
QY 1141 ACTCATATCCCAAAACCCATATACATCACTCACTGATCCTCTGTGATCAAGACCC 1200  
DB 1144 ACTCATATCCCAAAACCCATATACATCACTCACTGATCCTCTGTGATCAAGACCC 1203  
QY 1201 TCTCTCTGCTGAGTGTGCTCTTACCTCAATTCCTGGGATGGAGAGAGAGTGGC 1260  
DB 1204 TCTCTCTGCTGAGTGTGCTCTTACCTCAATTCCTGGGATGGAGAGAGAGTGGC 1263  
QY 1261 TTTTGTGGGCAATGCTTAACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1320  
DB 1264 TTTTGTGGGCAATGCTTAACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC 1323  
QY 1321 TGGAACTTCATCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGA 1380  
DB 1324 TGGAACTTCATCCACTCTTGTATGACTCCACAGTGTCCAGACTAATTTGTGATGA 1383  
QY 1381 CTGAAATTAACCATCTTACGATATCCAGGAAACAGAAAGCAGATGCGAGTGGAGGA 1440  
DB 1384 CTGAAATTAACCATCTTACGATATCCAGGAAACAGAAAGCAGATGCGAGTGGAGGA 1443  
QY 1441 CAGGAAGGAGCTGGGACATTTTAAAAATA 1472  
DB 1444 CAGGAAGGAGCTGGGACATTTTAAAAATA 1475

RESULT 15  
US-10-123-904-491  
; Sequence 491, Application US/10123904  
; Publication No. US20030022328A1  
; GENERAL INFORMATION:



APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Geriltsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Matanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P330R1C54  
 CURRENT APPLICATION NUMBER: US/10/123,904  
 CURRENT FILING DATE: 2002-04-16  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 491  
 LENGTH: 1475  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-123-904-491

Query Match 53.7%; Score 1472; DB 14; Length 1475;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 60  
 4 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTAAGAGTGTTCAGAGCAAGA 63  
 61 GCTTACGCTGAGAGCAAGGAGAGGAGTCCCTGAAGAGGCTTCTAGAGAGTCTGCAT 120  
 64 GCTTACGCTGAGAGCAAGGAGAGGAGTCCCTGAAGAGGCTTCTAGAGAGTCTGCAT 123  
 121 GGCCTCTCTGGCTCCCACTGTTGAGCTACATCTGAGGCTTCTGAGGCTTTTGGGAC 180  
 124 GGCCTCTCTGGCTCCCACTGTTGAGCTACATCTGAGGCTTCTGAGGCTTTTGGGAC 183  
 181 ACTGTTGCGATGCTGCTCCCACTGAGGAGGAGTCTTATGTTGAGTGGTCCAGATTGT 240  
 184 ACTGTTGCGATGCTGCTCCCACTGAGGAGGAGTCTTATGTTGAGTGGTCCAGATTGT 243  
 241 GACAGAGTGGCTTCTCCCAAGGCTCTGATGGAATGTCACACACAGACAGGAGCAT 300  
 244 GACAGAGTGGCTTCTCCCAAGGCTCTGATGGAATGTCACACACAGACAGGAGCAT 303  
 301 CACCAAGTGAACATCTATAGCACTTCTGAGGCTGCGCTGACATCCAGGCTGCGCA 360  
 304 CACCAAGTGAACATCTATAGCACTTCTGAGGCTGCGCTGACATCCAGGCTGCGCA 363  
 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 364 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423  
 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 424 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
 481 TGAGATCTTTTCACTCTGAGAGGCTCTGAGATTCATTCCTGTTGCTGGAATCTTCA 540  
 484 TGAGATCTTTTCACTCTGAGAGGCTCTGAGATTCATTCCTGTTGCTGGAATCTTCA 543  
 541 TGAGATCTTACGAGGATCTTCACTGAGATTCATTCCTGTTGCTGGAATCTTCA 600  
 544 TGAGATCTTACGAGGATCTTCACTGAGATTCATTCCTGTTGCTGGAATCTTCA 603

601 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATAGTGAATCACTT 660  
 604 AGAGGCTCTTACTTGGGATTAATTTCTTCCCTGTTCTCCCTGATAGTGAATCACTT 663  
 661 CTGCTTTTCTGCTACTTCCAGAGAAATGCTCAACTGATGATGATGATGATGATGATGAT 720  
 664 CTGCTTTTCTGCTACTTCCAGAGAAATGCTCAACTGATGATGATGATGATGATGATGAT 723  
 721 ACCTTGTGCAAGAGAGCTTCCAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 780  
 724 ACCTTGTGCAAGAGAGCTTCCAGAGCTGCTGATGATGATGATGATGATGATGATGATGAT 783  
 781 CAATTCCTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 784 CAATTCCTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843  
 841 TGGGTCGTGAAAG 900  
 844 TGGGTCGTGAAAG 903  
 901 GATTCGTGCAAG 960  
 904 GATTCGTGCAAG 963  
 961 GCAAGATGAG 1020  
 964 GCAAGATGAG 1023  
 1021 CAGCTTTTCTGTTTCTCACTGTTGCTGCTCCCTGATGATGATGATGATGATGATGATGAT 1080  
 1024 CAGCTTTTCTGTTTCTCACTGTTGCTGCTCCCTGATGATGATGATGATGATGATGATGAT 1083  
 1081 GAAACCCCATTTCTTCAAG 1140  
 1084 GAAACCCCATTTCTTCAAG 1143  
 1141 ACTCAATCCCAAG 1200  
 1144 ACTCAATCCCAAG 1203  
 1201 TCTCTGCTGAGTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 1204 TCTCTGCTGAGTGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263  
 1261 TTTTGTGGGATGCTTCAACTTCTCAAGCTTCTCCCAAGAGAGAGAGAGAGAGAGAGAG 1320  
 1264 TTTTGTGGGATGCTTCAACTTCTCAAGCTTCTCCCAAGAGAGAGAGAGAGAGAGAGAG 1323  
 1321 TGAACCTCAGTCCCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 1324 TGAACCTCAGTCCCACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383  
 1381 CTGAAATTAAG 1440  
 1384 CTGAAATTAAG 1443  
 1441 CAGGAAGGAGCTGAGAGATTTAAAAATA 1472  
 1444 CAGGAAGGAGCTGAGAGATTTAAAAATA 1475

Search completed: October 30, 2004, 18:00:41  
 Job time : 1798 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 11:47:04 ; Search time 12495 Seconds  
(without alignments)  
7996.618 Million cell updates/sec

Title: US-09-787-677A-7

Perfect score: 2742  
Sequence: 1 aagaatcagcctgcgcagaga.....ggtgatcaataatcctgac 2742

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219655908 residues

Word size : 20

Total number of hits satisfying chosen parameters: 936

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gsa1: \*  
9: gb\_gsa2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	25.3	693	9 AY400251	AY400251 Homo sapi
2	690	25.2	822	4 BG386074	BG386074 602455248
3	643	23.5	680	2 BE304667	BE304667 601105783
4	588	21.4	693	9 AY400252	AY400252 Pan trogl
5	582	21.2	589	5 BU071883	BU071883 im5d11.y
6	572	20.9	662	4 BM791379	BM791379 K-EST0071
7	555	20.2	555	5 BU073403	BU073403 im5d11.x
8	537	19.6	728	4 BG325755	BG325755 602424466
9	500	18.2	810	4 BG427780	BG427780 602497154
10	493	18.0	494	4 BG385562	BG385562 602453858
11	491	17.9	945	2 BE513091	BE513091 601171545
12	474	17.3	788	6 CB999779	CB999779 AGENCOURT
13	468	17.1	485	5 BU073420	BU073420 im5f11.x
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15	457	16.7	459	6 CA389170	CA389170 c806d06.y
16	457	16.7	454	5 BX096908	BX096908 BX096908
17	440	16.0	978	4 BG164062	BG164062 602341087
18	433	15.8	546	2 BF819923	BF819923 MRI-RT002
19	424	15.5	477	4 BM791008	BM791008 K-EST0070
20	420	15.3	420	1 AI343787	AI343787 qp12b03.x
21	420	15.3	557	4 BG399901	BG399901 602441435
22	420	15.3	623	2 AM837724	AM837724 CML-LT004
23	408	14.9	1025	2 BE249990	BE249990 600943168
24	407	14.8	407	1 AI285131	AI285131 qk57a09.x

C 25	403	14.7	448	1 AA973123	AA973123 OP45F04.8
C 26	394	14.4	511	1 AM006504	AM006504 w05e05.x
C 27	373	13.6	374	2 AW351531	AW351531 IL2-CT003
C 28	350	12.8	652	7 CR628947	CR628947 DKFZp469L
C 29	349	12.7	650	7 CR546700	CR546700 DKFZp470L
C 30	348	12.7	424	2 AM361715	AM361715 PM0-CT026
C 31	334	12.2	446	2 BE048787	BE048787 hr53e12.x
C 32	330	12.0	420	2 AM015998	AM015998 UI-H-B10P
C 33	323	11.8	341	4 BG985977	BG985977 CML-DT004
C 34	321	11.7	368	1 A1685788	A1685788 lu20f12.x
C 35	321	11.7	630	2 AM837727	AM837727 CML-LT004
C 36	313	11.4	391	2 AM083920	AM083920 xc25h04.x
C 37	307	11.2	420	5 BQ322242	BQ322242 RC4-CT084
C 38	302	11.0	302	1 A1465683	A1465683 cm20a03.x
C 39	301	11.0	301	1 A1244378	A1244378 qj76d10.x
C 40	300	10.9	300	1 A1659323	A1659323 lu29p10.x
C 41	300	10.9	300	1 A1685439	A1685439 t88c07.x
C 42	297	10.8	297	4 BM852012	BM852012 K-EST0133
C 43	294	10.7	396	1 A1949846	A1949846 wg14e11.x
C 44	290	10.6	1043	4 BG164241	BG164241 602341250
C 45	288	10.5	361	2 AW938611	AW938611 PM1-DT006

#### ALIGNMENTS

RESULT 1  
LOCUS AY400251  
DEFINITION Homo sapiens C12D2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
ACCSSION AY400251  
VERSION AY400251.1 GI:39756240  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
Gene trios  
Inferred nonneutral evolution from human-chimp-mouse orthologous  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE  
Direct Submision  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment  
FEATURES  
source  
Location/Qualifiers  
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Query Match 25.3%; Score 693; DB 9; Length 693;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGCCCTCTCTGGCCCTCCAACTTGAGGGCTACATCCAGGCCCTTCTG363CTTTTG36C 60  
 QY 179 ACATGGTGGCCAGTGTGTCTCCCAAGCTGGAAAAAGATTCTTATGTGGTGCAGAGCAT 238  
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 QY 359 CAGGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 418  
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 QY 419 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 478  
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 QY 479 GGTGGAGTCTTTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTC 538  
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 Db 421 CATGGATCTTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTC 480  
 QY 599 GAGAGGCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 658  
 Db 481 GAGAGGCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 540  
 QY 659 CTCTGCTTTTCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 718  
 Db 541 CTCTGCTTTTCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 600  
 QY 719 CAACCTCTTTCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 778  
 Db 601 CAACCTCTTTCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 660  
 QY 779 TTCAATTCCTACAGCCTGACAGGCTATGTGA 811  
 Db 661 TTCAATTCCTACAGCCTGACAGGCTATGTGA 693

RESULT 2  
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 LOCUS 602455248F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:4583675 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BG386074  
 VERSION BG386074.1 GI:13279520  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 822)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaubs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1CM1307 row: p column: 12

FEATURES High quality sequence stop: 746.  
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 /note="Organ: colon; Vector: pORF7; Site:1; XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAAGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)"

## ORIGIN

Query Match 25.2%; Score 690; DB 4; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGTACGCTGGCAGAGACTGTGAATAGGAGATTAGAGTCTTCAAGAGCAAG 60  
 Db 9 AGAAGTACGCTGGCAGAGACTGTGAATAGGAGATTAGAGTCTTCAAGAGCAAG 68  
 QY 61 GCTTCAGCCTGAAAG 120  
 Db 69 GCTTCAGCCTGAAAG 128  
 QY 121 GGCCTCTCTGAGCCTCAACTGTGGGCTACATCTTACAGGCTTTTGAGGAC 180  
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 QY 181 ACTGTTGCCAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 240  
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 QY 241 GAGAGAGAGTGGTTTCTCAAGAGGCTCTGAGTGAATGTGCACACAGCAGAGCAT 300  
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 QY 301 CACCAAGTGAATATATAGACACCTCTGAGGCTGCGCGTGAATCAGGCTGCCA 360  
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 QY 361 GGCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 Db 369 GGCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 428  
 QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
 Db 429 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 488  
 QY 481 TGGAGTCTTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 540  
 Db 489 TGGAGTCTTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 548  
 QY 541 TGGAGTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 600  
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 QY 601 AGAGGCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 660  
 Db 609 AGAGGCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 668  
 QY 661 CTGCTTTCTGCTCATCCAGAGAAATG 690  
 Db 669 CTGCTTTCTGCTCATCCAGAGAAATG 698

RESULT 3  
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LOCUS  
DEFINITION  
680 bp mRNA linear EST 13-JUL-2000  
601105763F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:2988309 5',  
mRNA sequence.  
ACCESSION  
BE304667  
VERSION  
BE304667.1 GI:9176036  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 680)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
AUTHORS  
Contact: Robert Strausberg, Ph.D.  
Email: cgsabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
COMMENT  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: NIH Intramural Sequencing Center  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: L16M77 row: f column: 22  
High quality sequence start: 27  
High quality sequence stop: 680.  
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/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN  
Query Match 23.5%; Score 643; DB 2; Length 680;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 GTGCGTCCAGCATTTGACAGCAGTTGCTTCCAGAGGCTCTGTGATGGAATGTC 283  
DB 38 GTCGGTCCAGCATTTGACAGCAGTTGCTTCCAGAGGCTCTGTGATGGAATGTC 97  
QY 284 ACAACAGCAGCAGGATCACCAGTGTGACATATAGCACCCTTGGGCTGCGCGCT 343  
DB 98 ACAACAGCAGCAGGATCACCAGTGTGACATATAGCACCCTTGGGCTGCGCGCT 157  
QY 344 GACATTCAGGCTGCGCGCATGATGTGATCATTCAGTCAATCTCTCCCTGAGCTGC 403  
DB 158 GACATTCAGGCTGCGCGCATGATGTGATCATTCAGTCAATCTCTCCCTGAGCTGC 217  
QY 404 ATTATCTGTGTGGGATGATGACAGTCTTTCGCCAGGAATCCCGAGCCAAAGAC 463  
DB 218 ATTATCTGTGTGGGATGATGACAGTCTTTCGCCAGGAATCCCGAGCCAAAGAC 277  
QY 464 AGATGCGGATGAGAGAGGAGTCTTTTTCATCCCTGGAGGCTCCCGGATTCATTCCT 523  
DB 278 AGATGCGGATGAGAGAGGAGTCTTTTTCATCCCTGGAGGCTCCCGGATTCATTCCT 337  
QY 524 GTTCCCTGGAATCTTTCATGAGGATCTTACGAGGATCTTACTACACCACTGGTCTGACAGC 583  
DB 338 GTTCCCTGGAATCTTTCATGAGGATCTTACGAGGATCTTACTACACCACTGGTCTGACAGC 397

QY 584 ATGAAATTTGAGATTGAGAGGCTCTTTACTTGGGATTAATTTCTCCCTGTTCCCTG 643  
DB 398 ATGAAATTTGAGATTGAGAGGCTCTTTACTTGGGATTAATTTCTCCCTGTTCCCTG 457  
QY 644 ATAGCTGAATCATCTCTGCTTTTCTGCTGATATCCCAAGAAATGCTCCAACTCTAC 703  
DB 458 ATAGCTGAATCATCTCTGCTTTTCTGCTGATATCCCAAGAAATGCTCCAACTCTAC 517  
QY 704 GATGCTTACCAAGCCCAACCTCTTGCACAGAGGCTCTCAAGGCTGATCACTCC 763  
DB 518 GATGCTTACCAAGCCCAACCTCTTGCACAGAGGCTCTCAAGGCTGATCACTCC 577  
QY 764 AAGTCAGAGTGAATTCATTCCTACAGCTGACAGGATGTGTGAAGAACAGGAGC 823  
DB 578 AAGTCAGAGTGAATTCATTCCTACAGCTGACAGGATGTGTGAAGAACAGGAGC 637  
QY 824 CAGAGCTGGGGGCTGCTGCTGTGTGAAAACAGTGCACAGC 866  
DB 638 CAGAGCTGGGGGCTGCTGCTGTGTGAAAACAGTGCACAGC 680

RESULT 4  
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LOCUS  
DEFINITION  
693 bp DNA linear GSS 15-DEC-2003  
Pan troglodytes CLDN2 gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY400252  
VERSION  
AY400252.1 GI:39756241  
KEYWORDS  
GSS.  
SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE  
1 (bases 1 to 693)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 693)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.5e-295; Indels 0; Gaps 0;  
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 GTGCGTCCAGCATTTGACAGCAGTTGCTTCCAGAGGCTCTGTGATGGAATGTC 283  
DB 106 GTGCGTCCAGCATTTGACAGCAGTTGCTTCCAGAGGCTCTGTGATGGAATGTC 165  
QY 284 ACAACAGCAGCAGGATCACCAGTGTGACATATAGCACCCTTGGGCTGCGCGCT 343

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Oy	344	GACATCCAGGCTGCCAGGCCCATAATGTGTGAATCATCAGTGCAATCTCTCTCCCTGGCTGGC		403
Db	226	GACATCCAGGCTGCCAGGCCCAGTGTGTGTGTGATCATCAGTGCAATCTCTCTCCCTGGCTGGC		285
Oy	404	ATTATCTCTGTGTGTGGGAGCATGAGATGACAGTCTTCTGACCAGAAATCCGAGCCAAGAAGC		463
Db	286	ATTATCTCTGTGTGTGGGAGCATGAGATGACAGTCTTCTGACAGAAATCCGAGCCAAGAAGC		345
Oy	464	AGAGTGGCGGTGACAGGTTGGAGATCTTTTTTATCTTGTGAGAGCTCTGTGGAAATTCATTCCT		523
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Oy	524	GTTGGCTTGAATCTTCATGGGAATCCGAGGAGCTTCTACTACACA CTGGTGCCTGACAGC		583
Db	406	GTTGGCTTGAATCTTCATGGGAATCCGAGGAGCTTCTACTACACA CTGGTGCCTGACAGC		465
Oy	584	ATGAATAATTGAGATTGAGAGGCTCTTTA CTTGGGCAATTATTCCTCTGTTCTCCCTG		643
Db	466	ATGAATAATTGAGATTGAGAGGCTCTTTA CTTGGGCAATTATTCCTCTGTTCTCCCTG		525
Oy	644	ATAGCTGAATCATCT		703
Db	526	ATAGCTGAATCATCT		585
Oy	704	GATGCGCTACCAAGCCCAACCTCTTGTGCCACAGAGAGCTCTCCAGAGCCTGTGTAACCTCC		763
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Oy	764	AAAGTCAGAGAGTAGTCAATTCCTACACGCTGACAGGGTATGTGTGA		811
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DEFINITION	BU071883	569 bp mRNA linear EST 27-AUG-2007		
ACCESSION	U555d11.y1	Human Insulinoma Homo sapiens cDNA clone IMAGE:6036933		
VERSION	BU071883			
KEYWORDS	BU071883.1 GI:22513072			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Euxariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 589) Melton,D., Brown,J., Kently,G., Pennmut,A., Lee,C., Kaestner,K., Lentelha,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Warte,M., Page,D., Wyile,T., Martin,J., Bliscain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000) Other ESTs: U555d11.x1 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@ionp.harvard.edu Library was constructed by Dr. J. Ferrer in vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@m.wustl.edu) Seq primer: -40RP from Gibco High quality sequence atop: 429. Location/Qualifiers 1..589			
TITLE	JOURNAL			
COMMENT				
FEATURES	source			

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		/clone_id="Human insulinoma"
		/note="Organ: pancreas; Vector: plasmid SK-; Site: 1; XhoI; Site 2: EcoRI; Constructed with lambda ZapII system (Stratagene) by Dr. J. Ferrer, in vivo mass-extracted to plasmid SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambdaprotocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
ORIGIN		
Query Match	21.2%; Score 582;	DB 5; Length 589;
Best Local Similarity	100.0%;	Pred. No. 3,4e-292;
Matches	582; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Oy	920	TGCTGAGGATGACTGACTTTGGCATTTGATGAGCAAAGGCCAATAAGGGGCTAGTG 979
Dd	68	TGCTGAGGATGACTGACTTTGGCATTTGATGAGCAAAGGCCAATAAGGGGCTAGTG 127
Oy	980	TAAACAGCAGTAGGATTGAATGCCAAGATGCTGCCATGCGACCTTTCTGTTTTCTC 10339
Dd	128	TAAACAGCAGTAGGATTGAATGCCAAGATGCTGCCATGCGACCTTTCTGTTTTCTC 187
Oy	1040	AACCTTGTCTGCTCCCTGCTTAATGCCAACCTTCAACTTGAATCCCATTTCCCTTAAG 10939
Dd	188	AACCTTGTCTGCTCCCTGCTTAATGCCAACCTTCAACTTGAATCCCATTTCCCTTAAG 247
Oy	1100	CCAGAAGCTCAGAGGATCCCTTTGGCTCTGTTTAACTGAGGACTCCATCCCACAACCAC 11559
Dd	248	CCAGAAGCTCAGAGGATCCCTTTGGCTCTGTTTAACTGAGGACTCCATCCCACAACCAC 307
Oy	1160	TAAATCACATCCCATGACTGACCTCTGTGATCAAAAGCCTCTCTCTGCTGAGGTTGG 1219
Dd	308	TAAATCACATCCCATGACTGACCTCTGTGATCAAAAGCCTCTCTCTGCTGAGGTTGG 367
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Dd	368	CTCTTAGCTCATGCTGCTGGGATGAGGAAGAGAACAGAGGCTTTTGGGGCATTGCTCTA 427
Oy	1280	ACCTACTTCTCAGAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTTCATCCCATC 1339
Dd	428	ACCTACTTCTCAGAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTTCATCCCATC 487
Oy	1340	TTTGTTTAACTCCCACTGCTCCAGATCTAATTTTGGCATGAACTGAATTAACAATCCTA 1359
Dd	488	TTTGTTTAACTCCCACTGCTCCAGATCTAATTTTGGCATGAACTGAATTAACAATCCTA 547
Oy	1400	CGGATATCAGAGGAACAGAAAGCAGATGACAGATGAGGAGAC 1441
Dd	548	CGGATATCAGAGGAACAGAAAGCAGATGACAGATGAGGAGAC 589
RESULT 6		
BM791379	662 bp	mRNA linear EST 05-MAR-2002
LOCUS	BM791379	
DEFINITION	K-EST0071366 S21SN0520 Homo sapiens cDNA clone S21SN0520-14-C06 5'	
ACCESSION	BM791379	
VERSION	BM791379.1	GI:19139611
KEYWORDS	EST.	

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 662)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongseung@mail.kribb.re.kr  
 Plate: 14 row: C column: 06  
 High quality sequence stop: 662.  
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 1..662  
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 /clone="S21SNV520-14-C06"  
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 /cell\_type="floating aggregates"  
 /cell\_line="SNU-520"  
 /lab\_host="Top10"  
 /clone\_lib="S21SNV520"  
 /note="Organ: Stomach; Vector: pTZ19BP1; Site 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10" by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

ORIGIN  
 Query Match 20.9%; Score 572; DB 4; Length 662;  
 Best Local Similarity 100.0%; Freq. No. 5.9e-287;  
 Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1685 TAGGGCACTGACCTGGCTCTTCTCTTAACCAACAAGGCTATAGACATGTT 1744  
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 Db 1 TAGGGCACTGACCTGGCTCTTCTCTTAACCAACAAGGCTATAGACATGTT 60  
 Oy 1745 TCCTTAGGAACAGTAAACAGATTTTCTAGGATGGCTTGGCTGGGGATGACAGTGT 1804  
 |||||  
 Db 61 TCCTTAGGAACAGTAAACAGATTTTCTAGGATGGCTTGGCTGGGGATGACAGTGT 120  
 Oy 1805 GGGAGCTGTGGGGATCTGAGGAAGACACATTCCTTGAACGCTCTTAAGAACCAAGTGTG 1864  
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 Db 121 GGGAGCTGTGGGGATCTGAGGAAGACACATTCCTTGAACGCTCTTAAGAACCAAGTGTG 180  
 Oy 1865 ATGTGTGTGGTCTCCAGTGGGTGTCTTACTCTGACAGTGAAGGAGCCCTTAGAA 1924  
 |||||  
 Db 181 ATGTGTGTGGTCTCCAGTGGGTGTCTTACTCTGACAGTGAAGGAGCCCTTAGAA 240  
 Oy 1925 ACTCTTAGGGCTAATGAAATCACTCAATATGATGAGTCCGCCGCCAGGCTCAACC 1984  
 |||||  
 Db 241 ACTCTTAGGGCTAATGAAATCACTCAATATGATGAGTCCGCCGCCAGGCTCAACC 300

Oy 1985 ACAGACACTACAGACCTCTTGAAAGACCAATAGACCAAGCCCTTCAGATTCGCC 2044  
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 Db 301 ACAGACACTACAGACCTCTTGAAAGACCAATAGACCAAGCCCTTCAGATTCGCC 360  
 Oy 2045 CACTGTCCATCGGAATATGCTCCAGATGGCTTAGAGGAGATCTTAAGGGCTCCAGATGGC 2104  
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 Db 361 CACTGTCCATCGGAATATGCTCCAGATGGCTTAGAGGAGATCTTAAGGGCTCCAGATGGC 420  
 Oy 2105 ATATCCATGCCCGGATGCTGTCTTCATGATCTGATGATAGCTGACCTGCTGGGGA 2164  
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 Db 421 ATATCCATGCCCGGATGCTGTCTTCATGATCTGATGATAGCTGACCTGCTGGGGA 480  
 Oy 2165 TTTCAGCTGAGTGGAGTGGAGTGAAGATGTTCCAGGAAGACAGTTCACCTTAAGGTC 2224  
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 Db 481 TTTCAGCTGAGTGGAGTGGAGTGAAGATGTTCCAGGAAGACAGTTCACCTTAAGGTC 540  
 Oy 2225 GAAATGTTCCCTTACCTCTGAGTGGAGTGG 2256  
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 Db 541 GAAATGTTCCCTTACCTCTGAGTGGAGTGG 572

RESULT 7  
 BU073403/c 555 bp mRNA linear EST 27-AUG-2002  
 LOCUS Im35d11.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6036933  
 DEFINITION 3', mRNA sequence.  
 ACCESSION BU073403  
 VERSION BU073403.1 GI:22514592  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 555)  
 AUTHORS Melton,D., Brown,D., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Seacore,M., Bresselli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Bilstain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,  
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.  
 TITLE Endocrine Pancreas Consortium  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@hbioph.harvard.edu  
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to  
 pluescript SK- by Dr. H. Inoue DNA sequencing by: Washington  
 University Genome Sequencing Center for information on obtaining a  
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 436.  
 FEATURES  
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 1..555  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6036933"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="Human Insulinoma"  
 /note="Organ: pancreas; Vector: pluescript SK-; Site 1:  
 XhoI; Site 2: EcoRI; Constructed with lambda ZapII system  
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to  
 pluescript SK- by Dr. H. Inoue following the Washington  
 University protocol  
 (http://genome.wustl.edu/sec/lambda\_protocol.shtml).  
 Please contact Hiroshi Inoue, MD/PhD for further  
 information on this library (Metabolism Division, Permutt

ORIGIN Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110. Note: this is a Washington University Pancreas EST project library."

Query Match 20.2%; Score 555; DB 5; Length 555;

Best Local Similarity 100.0%; Pred. No. 4.6e-278; Mismatches 0; Indels 0; Gaps 0;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 908 GTGAGAGGTCGTGAGTACGATGCTTGGCCATTGGATGAGCAAGGCAAAA 967

DB 555 GTGAGAGGTCGTGAGTACGATGCTTGGCCATTGGATGAGCAAGGCAAAA 496

QY 968 TGGGGGCTAGTGTACAGCATGAGTGTGAATGCGAAGATGCTCCGACAGCCTT 1027

DB 495 TGGGGGCTAGTGTACAGCATGAGTGTGAATGCGAAGATGCTCCGACAGCCTT 436

QY 1028 TGTGTTTCTCAGCTTGTGCTCCCTGCTTGAATGCGAAGATGCTCCGACAGCCTT 1087

DB 435 TGTGTTTCTCAGCTTGTGCTCCCTGCTTGAATGCGAAGATGCTCCGACAGCCTT 376

QY 1088 CATTCCTTAAAGCAGGAGTCAAGAGATCCCTTGGCTGCTGCTGCTGCTGCTGCT 1147

DB 375 CATTCCTTAAAGCAGGAGTCAAGAGATCCCTTGGCTGCTGCTGCTGCTGCTGCT 316

QY 1148 CCCCACCAACCATATACATATCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1207

DB 315 CCCCACCAACCATATACATATCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 256

QY 1208 GGGTGAAGTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267

DB 255 GGGTGAAGTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196

QY 1268 GGGTGAAGTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327

DB 195 GGGTGAAGTGGCTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 136

QY 1328 TCCATCCCACTCTTGTATGATCTCCAGTGTCCAGATATTTGTCATGAAT 1387

DB 135 TCCATCCCACTCTTGTATGATCTCCAGTGTCCAGATATTTGTCATGAAT 76

QY 1388 AAAACCATCTAGGATCCAGGAGACAGAAAGAGATGAGATGAGAGACAGAG 1447

DB 75 AAAACCATCTAGGATCCAGGAGACAGAAAGAGATGAGATGAGAGACAGAG 16

QY 1448 GCAGCCTGGAGCAT 1462

DB 15 GCAGCCTGGAGCAT 1

RESULT 8

BG325755 728 bp mRNA linear EST 27-FEB-2001

LOCUS 60244446F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4562273 5'

DEFINITION mRNA sequence.

ACCESSION BG325755

VERSION BG325755.1 GI:13132179

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

EXTRACTED FROM Human

REFERENCE 1 (bases 1 to 728)

TITLE NIH-MGC http://mgs.nci.nih.gov/

COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apds-remail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM1274 row: d column: 18  
High quality sequence stop: 708.

## FEATURES

## Source

1.728

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4562273"

/issue\_type="renal cell adenocarcinoma"

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/clone\_lib="NIH\_MGC\_14"

/note="Organ: Kidney; Vector: pOT7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(6) Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 19.6%; Score 537; DB 4; Length 728;

Best Local Similarity 100.0%; Pred. No. 1.2e-266; Mismatches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TTTGGGACACTGGTGGCATGCTGCTCCAGCTGGAACAAAGTTATGTCGTC 231

DB 82 TTTGGGACACTGGTGGCATGCTGCTCCAGCTGGAACAAAGTTATGTCGTC 141

QY 232 CAGCATTTGACAGCAGTGGCTTCTCCAGAGGCTCTGAGTGAATGTCACACAG 291

DB 142 CAGCATTTGACAGCAGTGGCTTCTCCAGAGGCTCTGAGTGAATGTCACACAG 201

QY 292 CAGAGCATCACCCAGTGGATGATCTATAGCAACCTTGGGCTCCGCTGACATCA 351

DB 202 CAGAGCATCACCCAGTGGATGATCTATAGCAACCTTGGGCTCCGCTGACATCA 261

QY 352 GGGTGGCAGGCGCATGATGGTGAATCTGATGATCTCTCCCTGGCTGATATCTC 411

DB 262 GGGTGGCAGGCGCATGATGGTGAATCTGATGATCTCTCCCTGGCTGATATCTC 321

QY 412 TGTGTGGGATGATGACAGTCTTCTGCGAGAAATCCGAGCAAGACAGAGTGC 471

DB 322 TGTGTGGGATGATGACAGTCTTCTGCGAGAAATCCGAGCAAGACAGAGTGC 381

QY 472 GGTAGCAGGTGATGATCTTTTCACTCTTGAAGGCTCTGAGATTTATCTGTCCTG 531

DB 382 GGTAGCAGGTGATGATCTTTTCACTCTTGAAGGCTCTGAGATTTATCTGTCCTG 441

QY 532 GAATCTTCAATGGATCTTACAGGATCTTACTACCACTGATGCTGACAGATGAAT 591

DB 442 GAATCTTCAATGGATCTTACAGGATCTTACTACCACTGATGCTGACAGATGAAT 501

QY 592 TGAATTTGAGAGAGCTCTTACTTGGGCAATATTTCTTCTGTTCTCCCTGATGCTG 651

DB 502 TGAATTTGAGAGAGCTCTTACTTGGGCAATATTTCTTCTGTTCTCCCTGATGCTG 561

QY 652 AATCATCTCTGCTTTTCTGCTGATCCAGAGAAATGCTCCAACTACTAGATGC 708

DB 562 AATCATCTCTGCTTTTCTGCTGATCCAGAGAAATGCTCCAACTACTAGATGC 618

RESULT 9

BG427780 810 bp mRNA linear EST 14-MAR-2001

LOCUS 602497154F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4610844 5'

DEFINITION mRNA sequence.

ACCESSION BG427780

VERSION BG427780.1 GI:13334286

KEYWORDS EST.

SOURCE Homo sapiens (human)



ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 810)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.llnl.gov  
 Plate: LICM1356 row: 1 column: 13  
 High quality sequence stop: 695.  
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 /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site: 1;  
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 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCCATTTAGGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.65  
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH-MGC Library."

Query Match 18.2%; Score 500; DB 4; Length 810;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-249;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

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1807 GAGCTGTGGGTAAGTGAAGACACCAATCTTTGAGGAGTGTCTAAGAACCCAGGTGAT 1866
1 GAGCTGTGGGTAAGTGAAGACACCAATCTTTGAGGAGTGTCTAAGAACCCAGGTGAT 60
1867 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1926
61 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
1927 TCTTGAAGGCGTAATGGAATCAGCTCAATAGATGATGAGGCCGCCCGAGGGTCCAGCCAC 1986
121 TCTTGAAGGCGTAATGGAATCAGCTCAATAGATGATGAGGCCGCCCGAGGGTCCAGCCAC 180
1987 AGAGCACTACAGAGCCTCTGAAAGACCATAGACCAAGCGAGCCCTTCAGATTCCCCCA 2046
181 AGAGCACTACAGAGCCTCTGAAAGACCATAGACCAAGCGAGCCCTTCAGATTCCCCCA 240
2047 CTGTCCATCGGAAGATGCTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2106
241 CTGTCCATCGGAAGATGCTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
2107 ATCCATGCGCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2166
301 ATCCATGCGCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
2167 GCAGCTGAGGTGAGTGAAGAAATGTTTCCAGAGAACAGATTCCACTTAAGGTCCGA 2226
361 GCAGCTGAGGTGAGTGAAGAAATGTTTCCAGAGAACAGATTCCACTTAAGGTCCGA 420
2227 AATGTTCCTTTTACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2286
421 AATGTTCCTTTTACCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 480

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ORIGIN

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2287 ACCAGTCTAGGATGACTGG 2306
481 ACCAGTCTAGGATGACTGG 500

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Query Match 18.0%; Score 493; DB 4; Length 494;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-245;  
 Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

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86 GTCCCTGAAGAGCTTCTAAGAGAGTGTGTGAGAGGCTCTGTGAGCTTCAAGTTGTG 145
2 GTCCCTGAAGAGCTTCTAAGAGAGTGTGTGAGAGGCTCTGTGAGCTTCAAGTTGTG 61
146 GGCTACATCTAGAGCTTCTGAGGCTTTTGGGACACTGAGTGTGCTGCTCCAGC 205
62 GGCTACATCTAGAGCTTCTGAGGCTTTTGGGACACTGAGTGTGCTGCTCCAGC 121
206 TGGAAAAAAGTTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 265
122 TGGAAAAAAGTTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 181
266 CTCTGAGTGAATGTGACACACACAGAGGATGACCAAGTGTGATCTATAGACAC 325
182 CTCTGAGTGAATGTGACACACACAGAGGATGACCAAGTGTGATCTATAGACAC 241
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FEATURES

source

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1. 494
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/note="Organ: colon; Vector: pOTB7; Site: 1; XhoI, Site: 2;  

EcoRI; cDNA made by oligo-dT priming. Directionally  

cloned into EcoRI/XhoI sites using the following 5'  

adaptor: GGACAGG(G). Size-selected >500bp for average  

insert size 1.8kb. Library constructed by Ling Hong in  

the laboratory of Gerald M. Rubin (University of  

California, Berkeley) using Zap-cDNA synthesis kit  

(Stratagene) and Superscript II RT (Life Technologies)"

```

REFERENCE 1 (bases 1 to 494)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.llnl.gov  
 Plate: LICM1304 row: C column: 15  
 High quality sequence stop: 493.  
 Location/Qualifiers  
 1. 494

Db 242 CTTCTGGGCGCTGCGCTGCATCCAGGCGCCAGCCATGATGTCATCCAGTGC 301  
Qy 386 ATTCCTCCCTGAGCTGATATCTCTGCTGGGCGATGATGCAAGCTCTGCGAG 445  
Db 302 ATTCCTCCCTGAGCTGATATCTCTGCTGGGCGATGATGCAAGCTCTGCGAG 361  
Qy 446 GAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGAGTCTTTTCATCTTGAAGGC 505  
Db 362 GAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGAGTCTTTTCATCTTGAAGGC 421  
Qy 506 CTCTCTGGATTCATCTCTGCTGCTGGAATCTTCATGAGGATCTTGAAGGACTTCTCA 565  
Db 422 CTCTCTGGATTCATCTCTGCTGCTGGAATCTTCATGAGGATCTTGAAGGACTTCTCA 481  
Qy 566 CCACGTGTGCTG 578  
Db 482 CCACGTGTGCTG 494

RESULT 11  
BE513091 945 bp mRNA linear EST 07-AUG-2000  
LOCUS BE513091 60171545F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:3545171 5',  
DEFINITION mRNA sequence.  
ACCESSION BE513091  
VERSION BE513091.1 GI:9720302  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgs.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: NIH Intramural Sequencing Center.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov  
Plate: LLCM241 row: 1 column: 12  
High quality sequence start: 36  
High quality sequence stop: 782.  
Location/Qualifiers

FEATURES  
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/organism="Homo sapiens"  
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/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adapter: GGCAAGAG(G). Size selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

## ORIGIN

Query Match 17.9%; Score 491; DB 2; Length 945;  
Best Local Similarity 100.0%; Pred. No. 1.5e-244;  
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTTGAGGTGTTCAAGAGCAAGA 60  
Db 69 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTTGAGGTGTTCAAGAGCAAGA 128

Qy 61 GCTTACGCTTGAAGACAGAGGACAGTCCCTTGAAGACGCTTTACTGAGAGGTCTGCCAT 120  
Db 129 GCTTACGCTTGAAGACAGAGGACAGTCCCTTGAAGACGCTTTACTGAGAGGTCTGCCAT 188  
Qy 121 GGCCTCTCTTGGCCTCCCACTTGTGGGCTACATCCCTAGAGCCTTCTGGGGCTTTTGGGCA 180  
Db 189 GGCCTCTCTTGGCCTCCCACTTGTGGGCTACATCCCTAGAGCCTTCTGGGGCTTTTGGGCA 248  
Qy 181 ACTGTTGTCATGCTGCTCCCAAGCTGGAACCAAGTTCTTATGTGTGTCAGCATTTGT 240  
Db 249 ACTGTTGTCATGCTGCTCCCAAGCTGGAACCAAGTTCTTATGTGTGTCAGCATTTGT 308  
Qy 241 GACAGAGTTGGCTTCTCAAGGGCTCTGATGATGTGCAACACAGACAGAGCAT 300  
Db 309 GACAGAGTTGGCTTCTCAAGGGCTCTGATGATGTGCAACACAGACAGAGCAT 368  
Qy 301 CACCCAGTGTGACATCTATAGCAACCTTGTGGGCTCCCGCTGACATCAGGCTGGCCA 360  
Db 369 CACCCAGTGTGACATCTATAGCAACCTTGTGGGCTCCCGCTGACATCAGGCTGGCCA 428  
Qy 361 GGCATGATGTGACATCCAGTGCATCTCTCCCTGAGCTGATATCTCTGTGTGGG 420  
Db 429 GGCATGATGTGACATCCAGTGCATCTCTCCCTGAGCTGATATCTCTGTGTGGG 488  
Qy 421 CATGATGTCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGGTAGCAG 480  
Db 489 CATGATGTCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGGTAGCAG 548  
Qy 481 TGGAGTCTTTT 491  
Db 549 TGGAGTCTTTT 559

RESULT 12  
CB999779 758 bp mRNA linear EST 01-MAY-2003  
LOCUS CB999779 13642925 NIH\_MGC\_186 Homo sapiens cDNA clone  
DEFINITION IMAGE:30322852 5', mRNA sequence.  
ACCESSION CB999779  
VERSION CB999779.1 GI:30294299  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NIH-MGC http://mgs.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Clontech Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDCM124 row: 1 column: 05  
High quality sequence stop: 592.  
Location/Qualifiers

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/note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI  
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oligo-dT primed and directionally cloned. cDNA was  
prepared from a pooled samples of tissues from skin,



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DEFINITION      nk140b1.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1013449 3',
                  mRNA sequence.
ACCESSION       AA552647
VERSION         AA552647.1 GI:2322901
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE           Tumor Gene Index
JOURNAL         Unpublished (1997)
COMMENT         Contact: Robert Strausberg, Ph.D.
                  Email: cgaps-remail.nih.gov
                  Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
                  Emmert-Buck, M.D., Ph.D.
                  CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                  Ph.D.
                  CDNA Library Arraying: Greg Lennon, Ph.D.
                  DNA Sequencing by: Washington University Genome Sequencing Center
                  Clone distribution: NCI-CGAP clone distribution information can be
                  found through the I.M.A.G.E. Consortium/ILMIL ac:
                  www-bio.11nl.gov/bdrip/image/image.html
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                  High quality sequence stop: 439.
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    /note="Organ: colon; Vector: Bluescript SK-; Site: 1;
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    Oligo dT. Bulk colon villous adenoma. 5' adaptor sequence:
    5' GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'
    CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
ORIGIN
Query Match      16.7%; Score 459; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.6e-228;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1007 GATGCTGCGCATGCGACGCTTTTCTGTTCTCTCACTTGTGCTCCCTGCTAAGTCC 1066
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DB 399 CGAACCTCAACTTGAACCCCATTCCTTAAGCAGAGACTCAGAGATCCCTTGCCCT 340
QY 1127 CTGCTTACCTGGAGACTCATCCCAACCACTAATCACTGCACTGACCTCT 1186
DB 339 CTGCTTACCTGGAGACTCATCCCAACCACTAATCACTGCACTGACCTCT 280
QY 1187 GTGATCAAGAACCTCTCTCTGCTGAGTGGCTCTTAAGCTCACTGCTGGAGATGGGAA 1246
DB 279 GTGATCAAGAACCTCTCTCTGCTGAGTGGCTCTTAAGCTCACTGCTGGAGATGGGAA 220
QY 1247 GGAAGCACTGCTTTGTGGGATGCTAAGCTAATCTTCAAGCTCCCTCCAAAG 1306
DB 219 GGAAGCACTGCTTTGTGGGATGCTAAGCTAATCTTCAAGCTCCCTCCAAAG 160
QY 1307 AAATGATTTGGCCTGGAGACTCATCCCACTCTTTTATGATCTCCAGAGTCCAGACT 1366
DB 159 AAATGATTTGGCCTGGAGACTCATCCCACTCTTTTATGATCTCCAGAGTCCAGACT 100
QY 1367 AATTGTGATGAATGAAATAAACCATCTCAAGTATCCAGGAAACAGAAAGCAGAT 1426

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DB 99 AATTGTGATGAATGAAATAAACCATCTCTCAAGTATCCAGGAAACAGAAAGCAGAT 40
QY 1427 GCAGATGGGAGACAGAAAGCAGCTGGGACATTTAA 1465
DB 39 GCAGATGGGAGACAGAAAGCAGCTGGGACATTTAA 1
RESULT 15
LOCUS          CA389170
DEFINITION     CA389170 459 bp mRNA linear EST 06-NOV-2002
                cs060606.y1 Human Retinal pigment epithelium/choroid cDNA
                (un-normalized, unamplified): cs Homo sapiens cDNA clone cs060606
                5', mRNA sequence.
ACCESSION      CA389170
VERSION        CA389170.1 GI:24719072
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,
                Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
                Expressed sequence tag analysis of human RPE/choroid for the
                NIDBank Project: Over 6000 non-redundant transcripts, novel genes
                and splice variants
                Mol. Vis. 8 (4), 205-220 (2002)
JOURNAL        MEDLINE
PUBMED         22103460
COMMENT        Contact: Wistow G
                Section on Molecular Structure and Function
                National Eye Institute
                6/331, NIH, Bethesda, MD 20892-2740, USA
                Tel: 301 402 3452
                Fax: 301 406 0078
                Email: gwaem@helix.nih.gov
                Plate: 06 row: d column: 06
                Seq primer: M13Rpl reverse primer (ABI).
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    /db_xref="taxon:9606"
    /clone="cs060606"
    /tissue_type="RPE/choroid"
    /dev_stage="Adult"
    /lab_host="EMD108"
    /clone_1lb="Human Retinal pigment epithelium/choroid cDNA
    (un-normalized, unamplified): cs"
    /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
    eyes (75-80 years old) yielded approximately 600 mg of
    dissected RPE/choroid tissue. This in turn yielded 340 ug
    of total RNA and 7 ug of mRNA. A directionally cloned cDNA
    library in the pCMVSPORT6 vector was constructed at Life
    Technologies (Rockville, MD; now part of Invitrogen Corp),
    essentially following the protocols of the Superscript
    Plasmid System (Invitrogen Corp).
    <http://www.invitrogen.com/>. The library code
    designation was cs. For this library, cDNA inserts were
    cloned into the NotI/MluI sites of the vector. EST
    analysis was performed on the unamplified library at the
    NIH Intramural Sequencing Center (NISC). "
ORIGIN
Query Match      16.7%; Score 457; DB 6; Length 459;
Best Local Similarity 100.0%; Pred. No. 8.4e-227;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTAAGGTTTCAGAGCAAGA 60
DB 3 AGAAGTCAGCTGGCAGAGACTCTGAATGAGGATTAAGGTTTCAGAGCAAGA 62

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QY 61 GCTTCAGCCTGAGACAGAGGAGCAGTCCCTGGAAGAGCTTCTAATGAGAGGTCTGCCAT 120
DB 63 GCTTCAGCCTGAGACAGAGGAGCAGTCCCTGGAAGAGCTTCTAATGAGAGGTCTGCCAT 122
QY 121 GGCCTCTCTTGGGCTTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 180
DB 123 GGCCTCTCTTGGGCTTCCAACTTGTGGGCTACATCTAGGCTTCTGGGGCTTTTGGGCAC 182
QY 181 ACTGTTGCGCATGCTGCTCCCGCAGCTGGAAAACAAGTTCTTATGTGGGTGCGAGCATTTGT 240
DB 183 ACTGTTGCGCATGCTGCTCCCGCAGCTGGAAAACAAGTTCTTATGTGGGTGCGAGCATTTGT 242
QY 241 GACAGCAGTTGGCTTCTCCAAAGGGCCTCTGGATGGAATGTGCCACAACAGCACAAGGCAT 300
DB 243 GACAGCAGTTGGCTTCTCCAAAGGGCCTCTGGATGGAATGTGCCACAACAGCACAAGGCAT 302
QY 301 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGCCCCGCTGACATCCAGGCTGCCA 360
DB 303 CACCCAGTGTGACATCTATAGCAACCTTCTGGGCTGCCCCGCTGACATCCAGGCTGCCA 362
QY 361 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 363 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
QY 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457
DB 423 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 459
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Search completed: October 29, 2004, 04:49:20  
Job time : 1249 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 27, 2004, 06:55:26 ; Search time 155 Seconds

(without alignments)  
532.308 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174  
Sequence: 1 MSLGLVGLVYGLGLGLG.....PGQPKVSEFNSYLTGYV 230Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	230	2 AAY36181	AAY36181 Human sec
2	1174	100.0	230	3 AAY84609	AAY84609 A human m
3	1174	100.0	230	3 AAY99378	AAY99378 Human PRO
4	1174	100.0	230	4 AAB66127	AAB66127 Protein o
5	1174	100.0	230	4 AAE04207	AAE04207 Human gen
6	1174	100.0	230	4 AAU12417	AAU12417 Human PRO
7	1174	100.0	230	4 AAU09178	AAU09178 Human PRO
8	1174	100.0	230	4 AAB87565	AAB87565 Human PRO
9	1174	100.0	230	4 AAB88342	AAB88342 Human mem
10	1174	100.0	230	5 ABP67991	ABP67991 Human col
11	1174	100.0	230	5 ABG95890	ABG95890 Human sec
12	1174	100.0	230	5 ABB84912	ABB84912 Human PRO
13	1174	100.0	230	5 AAU76534	AAU76534 Tumour-as
14	1174	100.0	230	5 ABG64507	ABG64507 Human alb
15	1174	100.0	230	5 ABB04707	ABB04707 Human SP8
16	1174	100.0	230	5 ABB95518	ABB95518 Human ang
17	1174	100.0	230	6 ABO17861	ABO17861 Novel hum
18	1174	100.0	230	6 ABU81115	ABU81115 Human PRO
19	1174	100.0	230	6 ABU90915	ABU90915 Novel hum
20	1174	100.0	230	6 ABO33974	ABO33974 Human sec
21	1174	100.0	230	6 ABU71991	ABU71991 Novel hum
22	1174	100.0	230	6 ABU66815	ABU66815 Human PRO
23	1174	100.0	230	6 ABU71545	ABU71545 Human sec
24	1174	100.0	230	6 ABR47946	ABR47946 Human sec
25	1174	100.0	230	6 ABU59896	ABU59896 Novel sec

26	1174	100.0	230	6 ABU72326	ABU72326 Human PRO
27	1174	100.0	230	6 ABU90999	ABU90999 Human PRO
28	1174	100.0	230	6 ABO27320	ABO27320 Human sec
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30	1174	100.0	230	6 ABR00178	ABR00178 Human gen
31	1174	100.0	230	6 ABU92515	ABU92515 Human sec
32	1174	100.0	230	6 ABU81185	ABU81185 Human sec
33	1174	100.0	230	6 ABO53299	ABO53299 Novel hum
34	1174	100.0	230	6 ABU67091	ABU67091 Human sec
35	1174	100.0	230	6 ABU98302	ABU98302 Novel hum
36	1174	100.0	230	6 ABU89307	ABU89307 Novel hum
37	1174	100.0	230	6 ABU82514	ABU82514 Novel hum
38	1174	100.0	230	6 ABU96478	ABU96478 Human PRO
39	1174	100.0	230	6 ABU72148	ABU72148 Human PRO
40	1174	100.0	230	6 ADA46011	ADA46011 Novel hum
41	1174	100.0	230	6 ADA76442	ADA76442 Human PRO
42	1174	100.0	230	6 ADB17137	ADB17137 Human tta
43	1174	100.0	230	6 ADA19092	ADA19092 Human PRO
44	1174	100.0	230	6 ADA61715	ADA61715 Homo bapl
45	1174	100.0	230	6 ADB19500	ADB19500 Novel hum

## ALIGNMENTS

RESULT 1  
AAY36181

ID AAY36181 standard; protein; 230 AA.

XX AAY36181;

DT 23-SEP-1999 (first entry)



SQ Sequence 230 AA;

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 Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
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QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECAHSTG 60  
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 DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDFYSPVPSDKFEIGALYGIISLPSLIAGII 180  
 DB 121 GGVFFILGGLGFIPIVAMNHLGILRDFYSPVPSDKFEIGALYGIISLPSLIAGII 180  
 QY 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230  
 DB 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 2  
 AAY84609 standard; protein; 230 AA.  
 AAY84609;  
 25-JUL-2000 (first entry)

A human membrane associated organizational protein (HUNCT).

Human; membrane associated organizational protein; HUNCT;  
 cell proliferative disorder; cancer; autoimmune disorder;  
 inflammatory disorder; neurological disorder; developmental disorder;  
 vesicle trafficking; reproductive disorder; gastrointestinal disorder;  
 renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;  
 Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;  
 irritable bowel syndrome; allergy.

Homo sapiens.

Key Location/Qualifiers  
 Modified-site /note= "potential phosphorylation site"  
 Modified-site 62 /note= "potential phosphorylation site"  
 Domain 117..138  
 Modified-site /note= "transmembrane domain"  
 Modified-site 155 /note= "potential phosphorylation site"  
 Domain 164..182  
 Modified-site /note= "transmembrane domain"  
 Modified-site 187 /note= "potential phosphorylation site"  
 Modified-site 190 /note= "potential glycosylation site"  
 Modified-site 208 /note= "potential phosphorylation site"  
 Modified-site 224 /note= "potential phosphorylation site"  
 Modified-site /note= "potential phosphorylation site"

MO200018915-A2.  
 06-APR-2000.  
 23-SEP-1999; 99WO-US022082.  
 25-SEP-1998; 98US-0155215P.  
 13-OCT-1998; 98US-0155251P.  
 04-MAY-1999; 99US-0172228P.

PA (INCY-) INCYTE PHARM INC.  
 PI Yue H, Lai P, Corley NC, Guejler KJ, Baughn MR, Lu AD, Tang YF;  
 DR WPI; 2000-293154/25.  
 DR N-PSDB; AAA12585.

Human membrane associated organizational protein and nucleic acid  
 sequences useful in the diagnosis, treatment and prevention of cell  
 proliferative associated disorders e.g. cancer, rheumatoid arthritis and  
 Alzheimer's disease.

Claim 1; Page 76-77; 84p; English.

The present sequence represents a membrane associated organizational  
 protein (HUNCT). HUNCT is used for the diagnosis, treatment and  
 prevention of cell proliferative disorders including cancer and  
 autoimmune/inflammatory, neurological, developmental, vesicle  
 trafficking, reproductive, gastrointestinal and renal disorders. These  
 disorders may include atherosclerosis, leukaemia, allergies, rheumatoid  
 arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects,  
 renal failure and irritable bowel syndrome. A vector expressing HUNCT,  
 and an agonist of HUNCT can be used to treat or prevent a disorder  
 associated with decreased expression or activity of HUNCT. An antagonist  
 of HUNCT or a vector expressing the complement of a polynucleotide  
 encoding HUNCT can be used to treat or prevent a disorder associated with  
 increased expression or activity of HUNCT. Antibodies which bind HUNCT  
 can be used for diagnosis of disorders associated with HUNCT expression  
 or to monitor patients being treated with HUNCT, agonists, antagonists or  
 inhibitors of HUNCT. Assays are preferably carried out on body fluids  
 from a patient using radioimmunoassay, enzyme linked immunosorbent assays  
 or fluorescent activated cell sorting assays. Polynucleotides encoding  
 HUNCT are also used in hybridisation assays to determine absence,  
 presence, or excess expression of HUNCT and to monitor regulation of HUNCT  
 levels during disease therapy

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGSKGLMECAHSTG 60  
 QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDFYSPVPSDKFEIGALYGIISLPSLIAGII 180  
 DB 121 GGVFFILGGLGFIPIVAMNHLGILRDFYSPVPSDKFEIGALYGIISLPSLIAGII 180  
 QY 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230  
 DB 181 LCFSCSSQNRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV 230

RESULT 3  
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 AAY9378;  
 08-AUG-2000 (first entry)

Human PRO1356 (UNQ705) amino acid sequence SEQ ID NO:134.

Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
 Homo sapiens.

XX WO200012708-A2.  
PN  
XX  
PD 09-MAR-2000.  
XX  
PF 01-SEP-1999; 99WO-US020111.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
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PR 03-SEP-1998; 98US-0099536P.  
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PR 09-SEP-1998; 98US-0099588P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099782P.  
PR 10-SEP-1998; 98US-0099808P.  
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PR 10-SEP-1998; 98US-0099815P.  
PR 15-SEP-1998; 98US-0099816P.  
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PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
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PR 16-SEP-1998; 98US-0100664P.  
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PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
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PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
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PR 07-OCT-1998; 98US-0103314P.  
  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
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PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 21-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 26-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105811P.  
PR 27-OCT-1998; 98US-0105822P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106566P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
  
(GETH ) GENENTECH INC.  
PA  
XX  
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;  
XX  
XX WPI: 2000-237871/20.  
DR N-PSDB; AAA37060.  
XX  
XX  
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
PT PRO polypeptides, useful for screening of potential peptide or small  
XX molecule inhibitors of the relevant receptor/ligand interactions.  
XX  
PS Claim 12, Fig 78; 773pp; English.  
XX  
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The  
CC transmembrane and receptor PRO proteins can be used for screening of

CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSVYGASIVTVAVGFSKGLMECATHTSG 60  
 DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSVYGASIVTVAVGFSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTLLGLPADIOAQAOMMTSSAISLACTISVGMKCTVFCQESRAKRVAVA 120  
 DB 61 ITQCDIYSTLLGLPADIOAQAOMMTSSAISLACTISVGMKCTVFCQESRAKRVAVA 120  
 QY 121 GGVFFILGILGLFIPVAMNLHGILRDYSPPLVPSDKMFEIGALYIGIISLPSLIAGII 180  
 DB 121 GGVFFILGILGLFIPVAMNLHGILRDYSPPLVPSDKMFEIGALYIGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

RESULT 4  
 AAB66127  
 ID AAB66127 standard; protein; 230 AA.

AC AAB66127;

DT 02-APR-2001 (first entry)

XX Protein of the invention #39.

KM Secreted; transmembrane; gene therapy.

XX Unidentified.

PN MO200078961-A1.

PD 28-DEC-2000.

PF 18-FEB-2000; 2000MO-US004342.

XX 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99MO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99MO-US028313.

PR 02-DEC-1999; 99MO-US028551.

PR 16-DEC-1999; 99MO-US030095.

PR 05-JAN-2000; 2000MO-US000219.

PR 06-JAN-2000; 2000MO-US000376.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

XX Williams PM, Wood WI;

XX WPI; 2001-071395/08.

PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.

XX Claim 1; Fig 78; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSVYGASIVTVAVGFSKGLMECATHTSG 60  
 DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSVYGASIVTVAVGFSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTLLGLPADIOAQAOMMTSSAISLACTISVGMKCTVFCQESRAKRVAVA 120  
 DB 61 ITQCDIYSTLLGLPADIOAQAOMMTSSAISLACTISVGMKCTVFCQESRAKRVAVA 120  
 QY 121 GGVFFILGILGLFIPVAMNLHGILRDYSPPLVPSDKMFEIGALYIGIISLPSLIAGII 180  
 DB 121 GGVFFILGILGLFIPVAMNLHGILRDYSPPLVPSDKMFEIGALYIGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

RESULT 5

AAB04207  
 ID AAB04207 standard; protein; 230 AA.

AC AAB04207;

DT 09-AUG-2001 (first entry)

DE Human gene 10 encoded secreted protein HRP1H83, SEQ ID NO:62.

XX Human; secreted protein; proliferative disorder; cancer; tumour;

KM foetal abnormality; developmental abnormality; haematopoietic disorder;

KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KM inflammation; allergy; neurological disorder; Alzheimer's disease;

KM Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KM skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KM cardiovascular disorder; angiogenic disorder; kidney disorder;

KM gastrointestinal disorder; pregnancy-related disorder; gene therapy;

KM endocrine disorder; infection; wound healing; vlnerary; cell culture;

KM chemotaxis; food additive; binding partner identification.

XX Homo sapiens.

OS Key

XX Peptide

FT 1..24

FT /label= signal\_peptide

FT Protein

FT 25..230

FT /note= "Mature secreted protein"

XX MO200136432-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000MO-US031162.

XX 19-NOV-1999; 99US-0166415P.

XX 30-JUN-2000; 2000US-0215136P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;  
 XX WPI; 2001-343793/36.  
 DR N-PSDB; AAD08497.  
 XX  
 PT Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.  
 XX  
 PS Claim 11; Page 439; 509pp; English.  
 XX  
 CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted  
 CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.  
 CC AAE04240-AAE04297 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new gene. Specific uses are described for each of the 18 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumors, foetal and developmental abnormalities,  
 CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infections. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin ageing due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The  
 CC present sequence represents a human secreted protein of the invention  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 1174; DB 4; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1, 1e-116;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASIGLQVGVYIGLGLGLTLVAMLLPSWKTSSYVAGSIYTAGVFSKGLMECATHTSG 60  
 Db 1 MASIGLQVGVYIGLGLGLTLVAMLLPSWKTSSYVAGSIYTAGVFSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTILGLPADIOAAQAMWVTSSAISLACIISVGMRTCTVCOESRADRYAVA 120  
 Db 61 ITQCDIYSTILGLPADIOAAQAMWVTSSAISLACIISVGMRTCTVCOESRADRYAVA 120  
 QY 121 GGVEFFIGLGLGFVPMNHLGLRDYSPVLPDSMKPEIGCALYLGITSLFLIAGII 180  
 Db 121 GGVEFFIGLGLGFVPMNHLGLRDYSPVLPDSMKPEIGCALYLGITSLFLIAGII 180  
 QY 181 LCFSSCSQNRNSNYDAYOAOPLATRSSPRGQPKYKSEFNSYSLNGYV 230  
 Db 181 LCFSSCSQNRNSNYDAYOAOPLATRSSPRGQPKYKSEFNSYSLNGYV 230  
 RESULT 6  
 AAU12417  
 ID AAU12417 standard; protein; 230 AA.  
 AC AAU12417;  
 XX  
 XX 24-OCT-2001 (first entry)  
 XX Human PRO1356 polypeptide sequence.  
 XX

KM Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KM prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KM ear; proliferation; tumour; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KM A-peptide; factor VIIa; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000MO-US032678.  
 XX  
 PR 01-DEC-1999; 99MO-US028301.  
 PR 01-DEC-1999; 99MO-US028634.  
 PR 02-DEC-1999; 99MO-US028551.  
 PR 02-DEC-1999; 99MO-US028564.  
 PR 02-DEC-1999; 99MO-US028565.  
 PR 02-DEC-1999; 99US-0170262P.  
 PR 16-DEC-1999; 99MO-US030095.  
 PR 20-DEC-1999; 99MO-US030911.  
 PR 20-DEC-1999; 99MO-US030999.  
 PR 30-DEC-1999; 99MO-US031243.  
 PR 30-DEC-1999; 99MO-US031274.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000277.  
 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004341.  
 PR 18-FEB-2000; 2000MO-US004342.  
 PR 22-FEB-2000; 2000MO-US004414.  
 PR 24-FEB-2000; 2000MO-US004914.  
 PR 01-MAR-2000; 2000MO-US005004.  
 PR 02-MAR-2000; 2000MO-US005601.  
 PR 03-MAR-2000; 2000MO-US005841.  
 PR 10-MAR-2000; 2000MO-US006319.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 20-MAR-2000; 2000MO-US007377.  
 PR 21-MAR-2000; 2000MO-US007532.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 11-AUG-2000; 2000MO-US022031.  
 PR 23-AUG-2000; 2000MO-US023522.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 10-NOV-2000; 2000MO-US030873.  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Bersini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAS21489.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
 PT breast, prostate, cervical.  
 XX  
 PS Claim 12; Fig 492; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful to detect other PRO  
 CC polypeptides, to link bioactive molecules to cells expressing PRO  
 CC polypeptides, to modulate biological activities of cells expressing PRO

CC polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. Some CC of the 275 sequences are also useful to stimulate the release of tumour CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the CC proliferation of inner ear utricular supporting cells or of T- CC lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO CC polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules CC involved in binding interactions. The polynucleotides encoding PRO CC transgenic or knock out animals and can be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITCCDIYSTLTGIPADIOAAQAMWVTSSAISLACITSVGMCCTVGCOSRAKDRVAVA 120  
DB 61 ITCCDIYSTLTGIPADIOAAQAMWVTSSAISLACITSVGMCCTVGCOSRAKDRVAVA 120  
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDFYSPVDPMSKFEIGALYIGIISLPSLIAGIT 180  
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDFYSPVDPMSKFEIGALYIGIISLPSLIAGIT 180  
QY 181 LCRCSSGQRNSVYDYQAQPLATRSSPRGPCKKSEFNSYSLTGYV 230  
DB 181 LCRCSSGQRNSVYDYQAQPLATRSSPRGPCKKSEFNSYSLTGYV 230

# RESULT 7

AAU09178  
ID AAU09178 standard; protein; 230 AA.

XX AAU09178;

XX 16-JAN-2002 (first entry)

XX Human PRO1356 polypeptide.

XX Human; PRO1356; clone DNA64886-1601; immune-related disorder;  
XX inflammatory disorder; infectious disorder; immunodeficiency disorder;  
XX autoimmune disorder; renal disease; demyelinating disease; skin disease;  
XX neoplasia; transplantation associated disease; immunosuppressive;  
XX anti-inflammatory; antiaesthetic; antidiabetic.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1..24 /label= Signal\_peptide

XX Modified-site 17..23 /note= "N-myristoylation site"

XX Modified-site 20..26 /note= "N-myristoylation site"

XX Protein 25..230 /label= Mature\_PRO1356\_polypeptide

XX Region 46..60 /note= "Also found in PMP-22, EMP and MP20 family proteins"

XX Modified-site 60..66 /note= "N-myristoylation site"

XX Domain 82..102

FT /label= Transmembrane\_domain  
FT 101..107 /note= "N-myristoylation site"  
FT Domain 117..140 /label= Transmembrane\_domain  
FT Modified-site 128..134 /note= "N-myristoylation site"  
FT Domain 153..182 /label= Transmembrane\_domain  
FT Modified-site 167..173 /note= "N-myristoylation site"  
FT Modified-site 178..184 /note= "N-myristoylation site"  
FT Modified-site 190..194 /note= "N-glycosylation site"  
FT Modified-site 216..225 /note= "Tyrosine kinase phosphorylation site"

XX WO200166740-A2.

XX 13-SEP-2001.

XX 01-MAR-2001; 2001WO-US006666.

XX 03-MAR-2000; 2000US-0187202P.  
XX 21-MAR-2000; 2000US-0191015P.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 01-DEC-2000; 2000WO-US032678.

XX (GETH ) GENENTECH INC.

XX Baton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

XX Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-625876/72.

XX N-PDB; AAS15360.

XX Nucleic acids encoding PRO polypeptides, useful for detecting and

XX treating immune related diseases and disorders in mammals including

XX autoimmune diseases, inflammatory diseases and asthma.

XX Claim 10; Fig 2; 122pp; English.

XX The present invention relates to the isolation of 9 novel human PRO  
XX polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.  
XX The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,  
XX PRO3151, PRO4332, PRO3964, PRO10008 and PRO19598. The cDNA sequences  
XX encoding these PRO polypeptides have been designated as clones DNA64886-  
XX 1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA92223-2567,  
XX DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.  
XX vaccines) containing PRO polypeptides and methods of using these  
XX compositions are useful in the treatment and diagnosis of immune-related  
XX disorders. Such disorders include immune-mediated inflammatory disorders  
XX (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.  
XX diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),  
XX immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.  
XX rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),  
XX demyelinating diseases of the peripheral or central nervous system (e.g.  
XX Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact  
XX dermatitis), neoplasias and transplantation associated diseases. The  
XX polynucleotide sequences of the invention may be used in gene therapy.  
XX AAU09178-AAU09186 represent the novel human PRO polypeptides of the  
XX invention

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60

```
Db      1 MASLGLQVLGVYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Qy      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIIISVGNKCTVFCQESRAKDRVAVA 120
Db      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIIISVGNKCTVFCQESRAKDRVAVA 120
Qy      121 GGVPFIIIGLGLGPIPVAMNHLGILRDYSPPLVPSDKMFEIAGEALYIGIISLFSLIAGII 180
Db      121 GGVPFIIIGLGLGPIPVAMNHLGILRDYSPPLVPSDKMFEIAGEALYIGIISLFSLIAGII 180
Qy      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPKVKSEFNSYSLTGYV 230
Db      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPKVKSEFNSYSLTGYV 230

RESULT 8
AAB87565
ID      AAB87565 standard; protein; 230 AA.
AC      AAB87565;
DT      15-MAY-2001 (first entry)
DE      Human PRO1356.
XX      Human; PRO protein; mapping.
XX      Homo sapiens.
XX      MO200116318-A2.
XX      08-MAR-2001.
XX      24-AUG-2000; 2000WO-US023328.
XX      01-SEP-1999; 99MO-US020111.
XX      15-SEP-1999; 99MO-US021090.
XX      07-DEC-1999; 99US-0169495P.
XX      09-DEC-1999; 99US-0170262P.
XX      11-JAN-2000; 2000US-0175481P.
XX      18-FEB-2000; 2000WO-US004341.
XX      18-FEB-2000; 2000WO-US004342.
XX      22-FEB-2000; 2000WO-US004414.
XX      01-MAR-2000; 2000WO-US005601.
XX      03-MAR-2000; 2000US-0187202P.
XX      21-MAR-2000; 2000US-0191007P.
XX      30-MAR-2000; 2000WO-US008439.
XX      25-APR-2000; 2000US-0199397P.
XX      22-MAY-2000; 2000WO-US014042.
XX      05-JUN-2000; 2000US-0209832P.
XX      (GETH ) GENENTECH INC.
XX      Baton DL, Flvaroff B, Gerritsen ME, Goddard A, Godowski PJ,
PI      Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,
XX      WPI, 2001-183260/18.
XX      N-PSDB; AAF92097.
XX      Bighey four nucleic acids encoding PRO polypeptides, useful in molecular
PT      biology, including use as hybridization probes, and in chromosome and
PT      gene mapping.
XX      Claim 12; Fig 80; 278pp; English.
XX      The present sequence is a human PRO polypeptide (secreted and
XX      transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX      anti-PRO antibodies are useful for preparation of a medicament useful in
XX      the treatment of a condition which is responsive to the PRO protein,
XX      CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX      employed as molecular weight markers for protein electrophoresis. The PRO
XX      coding sequence has applications in molecular biology, including use as
```

```
CC      hybridisation probes, and in chromosome and gene mapping
XX      SQ      Sequence 230 AA:
Qy      Query Match      100.0%; Score 1174; DB 4; Length 230;
Db      Best Local Similarity 100.0%; Pred. No. 1.1e-116;
Qy      Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      1 MASLGLQVLGVYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Qy      1 MASLGLQVLGVYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Db      1 MASLGLQVLGVYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAGFSKGLMECATHTSG 60
Qy      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIIISVGNKCTVFCQESRAKDRVAVA 120
Db      61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIIISVGNKCTVFCQESRAKDRVAVA 120
Qy      121 GGVPFIIIGLGLGPIPVAMNHLGILRDYSPPLVPSDKMFEIAGEALYIGIISLFSLIAGII 180
Db      121 GGVPFIIIGLGLGPIPVAMNHLGILRDYSPPLVPSDKMFEIAGEALYIGIISLFSLIAGII 180
Qy      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPKVKSEFNSYSLTGYV 230
Db      181 LCFSCSSQRRNSNYDAYOAOPLATRSSPRPGQPKVKSEFNSYSLTGYV 230

RESULT 9
AAB88342
ID      AAB88342 standard; protein; 230 AA.
AC      AAB88342;
DT      23-MAY-2001 (first entry)
DE      Human membrane or secretory protein clone PSEC0059.
XX      Human; secretory protein; membrane protein; vaccine; gene therapy;
XX      rheumatoid arthritis; diabetes.
XX      Homo sapiens.
XX      EP1067182-A2.
XX      10-JAN-2001.
XX      07-JUL-2000; 2000EP-00114090.
XX      08-JUL-1999; 99JP-00194179.
XX      11-JAN-2000; 2000JP-00118775.
XX      02-MAY-2000; 2000JP-00183766.
XX      (HELI-) HELIX RES INST.
XX      Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K,
PI      WPI, 2001-093989/11.
XX      N-PSDB; AAF93769.
XX      Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT      gene therapy or as candidate target molecules in drug development.
XX      Claim 1; SEQ ID NO 52; 609pp + Sequence Listing; English.
XX      This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX      which encode human secretory or membrane proteins represented by AAB88317
XX      CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
XX      CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
XX      CC invention. The invention also includes methods for the production of
XX      CC antibodies directed against the proteins, and cDNA sequences, which can
XX      CC be used in vaccines. The polynucleotide sequences can be used in gene
XX      CC therapy. The polynucleotide sequences and the proteins they encode may be
XX      CC used in the prevention, treatment and diagnosis of diseases associated
XX      CC with inappropriate secretory protein/membrane protein expression. The
XX      CC nucleic acids and complementary sequences may also be used as DNA probes
```

CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
CC and quantitate the presence of similar nucleic acid sequences in samples.  
CC They may also be used to study the expression and function of secretory  
CC proteins/membrane polypeptides and their role in metabolism. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC against them and in assays to identify modulators (agonists and  
CC antagonists) of expression and activity. The antibodies and antagonists  
CC may also be used as therapeutic agents to down regulate expression and  
CC activity. The antibodies may also be used as diagnostic agents for  
CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA). Examples of diseases which may be  
CC treated include rheumatoid arthritis and diabetes

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
DB 1 MASIGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKRVAVA 120  
QY 121 GGVFLLGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIAGII 180  
DB 121 GGVFLLGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIAGII 180  
QY 181 LCFSSCSQRRNSNYDAYQAOPLATRSSPPGQPPKVKSEFNYSYLTGYV 230  
DB 181 LCFSSCSQRRNSNYDAYQAOPLATRSSPPGQPPKVKSEFNYSYLTGYV 230

RESULT 10  
ABP67991

ID ABP67991 standard; protein; 230 AA.

XX AC ABP67991;

DT 13-DEC-2002 (first entry)

DE Human colon cancer related polypeptide SEQ ID NO 2590.

XX Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine.

OS Homo sapiens.

PN WO200258534-A2.

XX 01-AUG-2002.

PD 16-NOV-2001; 2001WO-US043704.

XX 20-NOV-2001; 2000US-0252222P.

PR 06-FEB-2001; 2001US-0267011P.

PR 28-MAR-2001; 2001US-0279670P.

PR 10-JUL-2001; 2001US-0304037P.

XX (CORI-) CORIXA CORP.

PA Stolk JA, Xu J, Chenault RA, Meagher MJ, Secrist H, King GE;

XX WPI; 2002-608400/65.

DR N-PSDB; ABV89278.

XX New isolated tumor colon-poly nucleotide and polypeptide, useful for the

PT diagnosis, prevention and/or treatment of cancer, in particular colon

PT cancer.

PS Claim 2; SEQ ID NO 2590; 266pp + Sequence Listing; English.

XX The invention relates to a human colon tumour expressed polynucleotide  
CC (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of  
CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)  
CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)  
CC sequences that hybridize to (i), under moderately stringent conditions;  
CC (v) sequences having at least 75% or 90% identity to (i); or (vi)  
CC degenerate variants of (i). The compositions and methods of the present  
CC invention are useful for the diagnosis, prevention and/or treatment of  
CC cancer, particularly colon cancer. (ii) can be used in gene therapy and  
CC (i) and (ii) are useful in pharmaceutical compositions such as vaccines.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 5; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
DB 1 MASIGQLVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAQAAMWVTSSAISLACIIISVGMKCTVFCQESRAKRVAVA 120  
QY 121 GGVFLLGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIAGII 180  
DB 121 GGVFLLGLGLGFIPTVAMNHLGILRDPYSPVPDSMKFEIGELALYGIISLPSLIAGII 180  
QY 181 LCFSSCSQRRNSNYDAYQAOPLATRSSPPGQPPKVKSEFNYSYLTGYV 230  
DB 181 LCFSSCSQRRNSNYDAYQAOPLATRSSPPGQPPKVKSEFNYSYLTGYV 230

RESULT 11  
ABG95890

ID ABG95890 standard; protein; 230 AA.

XX AC ABG95890;

DT 10-DEC-2002 (first entry)

DE Human secreted/transmembrane protein PRO1356.

XX Human; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;

KM articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

PN US2002119130-A1.

XX 29-AUG-2002.

PD 06-DEC-2001; 2001US-0006867.

XX 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0064215P.

PR 22-APR-1998; 98US-0082797P.

PR 29-APR-1998; 98US-0083495P.

PR 15-MAY-1998; 98US-0085579P.

PR 02-JUN-1998; 98US-0087599P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.



PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 25-JUN-1998; 98US-0090688P.  
 PR 25-JUN-1998; 98US-0090686P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 16-SEP-1998; 98US-0099815P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100652P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 17-SEP-1998; 98US-0100663P.  
 PR 17-SEP-1998; 98US-0100684P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 22-SEP-1998; 98US-0101279P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 30-SEP-1998; 98US-0101916P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 08-MAR-1999; 99US-00050528.  
 PR 14-MAY-1999; 99US-00010733.  
 PR 02-JUN-1999; 99US-00012252.  
 PR 01-SEP-1999; 99US-00020111.  
 PR 15-SEP-1999; 99US-00021090.  
 PR 15-SEP-1999; 99US-00021194.  
 PR 22-DEC-1999; 99US-00030720.  
 PR 18-FEB-2000; 2000US-0004341.  
 PR 18-FEB-2000; 2000US-0004342.  
 PR 22-FEB-2000; 2000US-0004414.  
 PR 01-MAR-2000; 2000US-0005601.  
 PR 30-MAR-2000; 2000US-0008439.  
 PR 22-MAY-2000; 2000US-0014042.  
 PR 02-JUN-2000; 2000US-0015264.  
 PR 23-AUG-2000; 2000US-0023522.  
 PR 24-AUG-2000; 2000US-0023328.  
 PR 10-NOV-2000; 2000US-0030873.  
 PR 01-DEC-2000; 2000US-0032378.  
 PR 20-DEC-2000; 2000US-0034356.  
 PR 28-FEB-2001; 2001US-0006520.  
 PR 01-MAR-2001; 2001US-0006666.  
 PR 30-MAY-2001; 2001US-0017443.  
 PR 01-JUN-2001; 2001US-0017800.  
 PR 20-JUN-2001; 2001US-0019692.  
 PR 29-JUN-2001; 2001US-0021066.  
 PR 09-JUL-2001; 2001US-0021735.  
 PR XX  
 PA (GETH ) GENENTECH INC.  
 PI Baton DL, Filvetroff E, Gerritsen ME, Goddard A, Godowski RJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI; 2002-731348/79.  
 DR N-PSDB; ABS74417.  
 XX

PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating sports-related  
 PT joint problems, osteoarthritis or rheumatoid arthritis.  
 PS Claim 20; Fig 80; 399pp; English.

XX  
 CC The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing as  
 CC ABG98851-ABG95934 or their associated signal peptide, or a sequence of an  
 CC extracellular domain of the proteins with their associated signal peptide  
 CC or lacking its associated signal peptide. Also included are the nucleic  
 CC acids encoding the proteins, vectors, host cells, fusion proteins and  
 CC antibodies which specifically bind to the proteins. The proteins are  
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
 CC suspected of containing an A, B, C or D polypeptide. By contacting the  
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide  
 CC conjugate in the sample, where the formation of the conjugate is  
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
 CC H or I polypeptide is labeled with a detectable label or is attached to a  
 CC solid support. The proteins are useful for linking a bioactive molecule  
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
 CC H or I. The bioactive molecule is a toxin, a radiolabel, or an antibody.  
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
 CC or I, or antibodies against them are useful for modulating a biological  
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
 CC identifying agonists or antagonists, for the preparation of a medicament  
 CC useful in the treatment of a condition which is responsive to the  
 CC proteins, as molecular weight markers for protein electrophoresis  
 CC purposes, and as therapeutic agents for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis. Nucleic acids encoding the proteins are useful as  
 CC hybridization probes, in chromosome and gene mapping, in the generation  
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
 CC generate transgenic or knockout animals which are useful in the  
 CC development and screening of therapeutic useful reagents, for chromosome  
 CC identification, and in gene therapy. The antibody is useful as a  
 CC therapeutic agent, in a diagnostic assay and for affinity purification of  
 CC the protein from recombinant cell culture natural sources. The present  
 CC sequence represents a novel secreted or transmembrane protein of the  
 CC invention  
 CC XX

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-116; Indels 0; Gaps 0;  
 Matches 230; Conservative 0; Mismatches 0;

QY 1 MASLGLVGYITGLGLTVAALLPSWKTSYVGAISVTPAVGSKGLMECAHSTG 60  
 Db 1 MASLGLVGYITGLGLTVAALLPSWKTSYVGAISVTPAVGSKGLMECAHSTG 60  
 QY ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTISVVGKCTVFCQESRAKQAVAA 120  
 Db ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTISVVGKCTVFCQESRAKQAVAA 120  
 QY 121 GGVFFILGLIGLPIPAVMNLHGILRPFYSPVVDKSKFEGELLYGIISSLSLNGIT 180  
 Db 121 GGVFFILGLIGLPIPAVMNLHGILRPFYSPVVDKSKFEGELLYGIISSLSLNGIT 180  
 QY 181 LCFSSCSQRNRKSNYYDAYOQPLATRSPPGQPKYKSEFNSYSLTGY 230  
 Db 181 LCFSSCSQRNRKSNYYDAYOQPLATRSPPGQPKYKSEFNSYSLTGY 230

RESULT 12  
 ABB84912

XX	AB884912 standard; protein; 230 AA.
AC	AB884912;
DT	16-MAY-2002 (first entry)
DE	Human PRO1356 protein sequence SEQ ID NO:192.
XX	
KW	Human; angiogenesis; cardiac; cytoskeletal; antiangiogenic; hypotensiv
KW	vulnerable; arteriole; arteriosclerotic; PRO agonist; PRO antagonist; trauma
KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer; K
KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension
KW	age-related atherosclerotic degeneration; arterial restenosis; angina;
KW	rheumatoid arthritis; myocardial infarction; thrombophilic; lymphangi
KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma
KW	wound healing; chromosome mapping; gene mapping.
XX	
OS	Homo sapiens.
XX	
PN	WO200200690-A2.
XX	
PD	03-JAN-2002.
XX	
PP	20-JUN-2001; 2001WO-US019692.
XX	
PR	23-JUN-2000; 2000US-0213637P.
PR	20-JUL-2000; 2000US-0219556P.
PR	25-JUL-2000; 2000US-0220524P.
PR	25-JUL-2000; 2000US-0220664P.
PR	28-JUL-2000; 2000WO-US020710.
PR	02-AUG-2000; 2000US-0222695P.
PR	17-AUG-2000; 2000US-00643657.
PR	23-AUG-2000; 2000WO-US023328.
PR	24-AUG-2000; 2000WO-US023328.
PR	07-SEP-2000; 2000US-0230978P.
PR	18-SEP-2000; 2000US-00664610.
PR	18-SEP-2000; 2000US-00665350.
PR	24-OCT-2000; 2000US-0242922P.
PR	08-NOV-2000; 2000US-00709232.
PR	08-NOV-2000; 2000WO-US030952.
PR	10-NOV-2000; 2000WO-US030873.
PR	01-DEC-2000; 2000WO-US032678.
PR	20-DEC-2000; 2000US-00747259.
PR	20-DEC-2000; 2000WO-US034956.
PR	22-JAN-2001; 2001US-00767609.
PR	28-FEB-2001; 2001US-00796498.
PR	28-FEB-2001; 2001WO-US006520.
PR	01-MAR-2001; 2001WO-US006666.
PR	09-MAR-2001; 2001US-00802706.
PR	14-MAR-2001; 2001US-00808669.
PR	22-MAR-2001; 2001US-00816744.
PR	05-APR-2001; 2001US-00828366.
PR	10-MAY-2001; 2001US-00854208.
PR	10-MAY-2001; 2001US-00854280.
PR	25-MAY-2001; 2001US-00866028.
PR	25-MAY-2001; 2001US-00866034.
PR	25-MAY-2001; 2001WO-US017092.
PR	30-MAY-2001; 2001US-00870574.
PR	30-MAY-2001; 2001WO-US017443.
PR	01-JUN-2001; 2001WO-US017800.
XX	
PA	(GETH ) GENENTECH INC.
XX	
PI	Baker KP, Ferrara N, Gether H, Gertlesen ME, Goddard A;
PI	Goodwell JF, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF
PI	Stephan PJ, Watson CK, Williams PM, Wood WI, Ye W;
XX	
DR	WPI; 2002-090516/12.
DR	N-PSDB; ABL88167.
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal.

XX	Claim 11; Fig 192; 565pp; English.
PS	
CC	AH88072 to AB8825 encode the PRO proteins given in AB884817 to
CC	AB885003. The PRO proteins and polynucleotides have carterant, cytostatic,
CC	antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agensets and antagonists are useful for treating or diagnosing
CC	a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC	cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC	angina, myocardial infarctions, thrombophilicities, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The PRO polynucleotides have applications in molecular biology,
CC	including use as hybridisation probes, and in chromosome and gene
CC	mapping. AB88259 to AB88267 represent primers and probes used in the
CC	exemplification of the present invention
XX	
SO	Sequence 230 AA;
	Query Match            100.0%; Score 1174; DB 5; Length 230;
	Best Local Similarity   100.0%; Pred. No. 1.1e-116;
	Matches   230; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
OY	1 MASIGLQVGIILGLIGLTIVAMLLPMSKTSSTVGASITVANGFSGKLMECATSTG 60
Db	1 MASIGLQVGIILGLIGLTIVAMLLPMSKTSSTVGASITVANGFSGKLMECATSTG 60
OY	ITGGDIYSTLLGLPADIQAAQAMWVTSSAISLACIIISVGMRICTVCQESRADRVAVA 120
Db	61 ITGGDIYSTLLGLPADIQAAQAMWVTSSAISLACIIISVGMRICTVCQESRADRVAVA 120
OY	121 GGVPFIILGGLIFIPVAMNHLGIIRDYSPLVPDSMKFEIGEALYLGIISLSFLINGII 180
Db	121 GGVPFIILGGLIFIPVAMNHLGIIRDYSPLVPDSMKFEIGEALYLGIISLSFLINGII 180
OY	181 LCFSCSSQRNSNYDAYQAQPLATRSSPRGCPPKKSSEFNSYSLGVY 230
Db	181 LCFSCSSQRNSNYDAYQAQPLATRSSPRGCPPKKSSEFNSYSLGVY 230
RESULT 13	
AAU76534	ID    AAU76534 standard; protein; 230 AA.
XX	
AC	AAU76534;
DT	05-JUN-2002 (first entry)
XX	
DE	Tumour-associated antigenic target protein, TAT134.
XX	
KM	TAT134, Tumour-associated Antigenic Target; tumour; breast cancer;
KM	colorectal cancer; lung cancer; ovarian cancer;
KW	central nervous system cancer; liver cancer; bladder cancer; melanoma;
KX	pancreatic cancer; leukaemia; gene therapy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Region
FT	Modified-site
FT	Modified-site
FT	Protein
FT	Modified-site
FT	Domain
	Location/Qualifiers
	/note= "Signal sequence"
	4..181
	/note= "PMP-32/BMP/MP20/Claudin family (not defined)"
	17..22
	/note= "N-myristoylation site"
	20..25
	/note= "N-myristoylation site"
	25..230
	/note= "Mature TAT134"
	60..65
	/note= "N-myristoylation site"
	82..102
	/note= "Transmembrane domain"

FT Modified-site 101..106  
FT /note="N-myristoylation site"  
FT Domain 120..140  
FT /note="Transmembrane domain"  
FT Modified-site 128..133  
FT /note="N-myristoylation site"  
FT Domain 160..180  
FT /note="Transmembrane domain"  
FT Modified-site 167..172  
FT /note="N-myristoylation site"  
FT Modified-site 178..183  
FT /note="N-myristoylation site"  
FT Modified-site 190..193  
FT /note="Asn is N-glycosylated"  
FT Modified-site 216..224  
FT /note="Tyrosine kinase phosphorylation site"  
XX WO200216429-A2.  
XX  
XX  
XX 28-FEB-2002.  
XX  
XX 22-JUN-2001; 2001WO-US020118.  
XX  
XX  
XX 24-AUG-2000; 2000WO-US023328.  
XX 26-SEP-2000; 2000US-0235451P.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 01-MAR-2001; 2001WO-US006666.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,  
XX Wood WI, Wu TD, Zhang Z;  
XX  
XX WPI; 2002-280917/32.  
XX N-PSDB; ABK11089.  
XX  
XX Novel isolated tumor-associated antigenic target polypeptides which are  
XX useful as targets for cancer therapy and diagnosis in mammals.  
XX  
XX Claim 12; Fig 6; 121pp; English.  
XX  
XX The invention relates to an isolated tumour-associated antigenic target  
XX polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the  
XX polynucleotides (II) encoding them. (II) is useful for diagnosing the  
XX presence of a tumour in a mammal, where the level of expression of (II)  
XX is indicative of the presence of tumour in the mammal from which the test  
XX sample was obtained. Antibody to (I) is useful for killing a cancer cell  
XX (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,  
XX an ovarian cancer cell, a central nervous system (CNS) cancer cell, a  
XX liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a  
XX melanoma cell or a leukemia cell) that expresses (I). Oligonucleotides  
XX hybridizing to (II) are useful as diagnostic probes, antisense  
XX oligonucleotide probes or for encoding fragments of full length TAT  
XX polypeptide. (II) is also useful in chromosome and gene mapping and in  
XX the generation of antisense RNA and DNA probes, for constructing  
XX hybridisation probes for mapping the gene encoding TAT and for genetic  
XX analysis of individuals with genetic disorders. (II) is also useful for  
XX generating either transgenic animals or knockout animals, and in gene  
XX therapy. The TAT polypeptides and nucleic acids may also be used for  
XX tissue typing and the TAT polypeptides are useful for screening compounds  
XX that mimic the TAT polypeptide (agonist) or prevent the effect of TAT  
XX polypeptide (antagonist). The antibody is useful for staging TAT  
XX polypeptide-expressing cancers, purifying or immunoprecipitating TAT  
XX polypeptide from cells, for detection and quantitation of TAT polypeptide  
XX in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or  
XX Western blot. The antibodies are also useful for treating a TAT-  
XX expressing cancer or alleviating one or more symptoms of cancer in a  
XX mammal. The present sequence represents the amino acid sequence of TAT134  
XX  
XX Sequence 230 AA;  
XX  
XX Query Match 100.0%; Score 1174; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASLGQLVGYIIGLLGLTGLVAMLLPQWKTSSYGAASIVFAVGSKGLMECAHTSTG 60  
DB 1 MASLGQLVGYIIGLLGLTGLVAMLLPQWKTSSYGAASIVFAVGSKGLMECAHTSTG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACTIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVPFLIGLGLGPIPVAMNHLGIRDPFSPVVDNSKPFEGELALYIGITISLPSLLAGIT 180  
DB 121 GGVPFLIGLGLGPIPVAMNHLGIRDPFSPVVDNSKPFEGELALYIGITISLPSLLAGIT 180  
QY 181 LCFSCSSQRNRSNRYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSCSSQRNRSNRYDAYOAOPLATRSSPPGQPPVKSEFNSYSLTGYV 230  
RESULT 14  
ABG64507 standard; protein; 230 AA.  
AC ABG64507;  
XX 27-AUG-2002 (first entry)  
DT XX  
DE Human albumin fusion protein #1182.  
XX  
XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
XX human serum albumin; HSA; cancer; reproductive disorder;  
XX digestive disorder; immune disorder; endocrine disorder;  
XX hematopoietic disorder; neural disorder; connective disorder;  
XX cytostatic; antifertility; antiinflammatory; anticler;  
XX immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
XX neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
XX osteopathic; antiarthritic.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200177137-A1.  
XX  
XX 18-OCT-2001.  
XX  
XX 12-APR-2001; 2001WO-US011988.  
XX  
XX 12-APR-2000; 2000US-0229358P.  
XX 25-APR-2000; 2000US-0199384P.  
XX 21-DEC-2000; 2000US-0256931P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2002-010886/01.  
XX  
XX New fusion protein for treating disease e.g. diabetes comprises an  
XX albumin fused to a therapeutic protein.  
XX  
XX Claim 1; Page 1277-1278; 2102pp; English.  
XX  
XX The present invention relates to albumin fusion proteins comprising a  
XX therapeutic protein X and human albumin (HA, also known as human serum  
XX albumin, HSA). The proteins are useful for treating a disease or disorder  
XX that may be modulated by therapeutic protein X. The albumin extends the  
XX shelf-life of protein X, and may increase its biological in vitro/in vivo  
XX activity. The protein is useful for treating and diagnosing disorders  
XX such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
XX disease, ulcerative colitis), immune disorders (e.g. acquired  
XX immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
XX hematopoietic disorders, neural disorders (e.g. Alzheimer's,

CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
XX  
SQ Sequence 230 AA:

Query Match 100.0%; Score 1174; DB 5; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
DB 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMRCCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMRCCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGBALYIGIISLFSLIAGII 180  
DB 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGBALYIGIISLFSLIAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYOAPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYYDAYOAPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230

RESULT 15

ABB04707 standard; protein; 230 AA.

AC ABB04707;

DT 11-MAR-2002 (first entry)

DE Human SP82 protein SEQ ID NO:2.

KW Human; SP82; cancer suppression.

OS Homo sapiens.

PN CN1313315-A.

PD 19-SEP-2001.

PF 13-MAR-2000; 2000CN-00111989.

PR 13-MAR-2000; 2000CN-00111989.

PA (SHAN-) SHANGHAI INST ONCOLOGY.

PI Gu J, Yang S;

DR WPI, 2002-042193/06.

DR N-PSDB; ABA0424.

PT New human protein able to suppress growth of cancer cells and its  
encoding polynucleotide sequence.

PS Claim 1; Page 12 (Disclosure); 42pp; Chinese.

CC The present sequence represents human SP82 protein, which has cancer-  
suppressing activity. The present invention also describes a method for  
the preparation of the protein by recombination, and the application of  
the protein in treating diseases such as cancer

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 5; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMMECATHTSG 60

DB 1 MASLGQLVGYILGLGLTLVAMLLPSMKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMRCCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIIISVGMRCCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGBALYIGIISLFSLIAGII 180  
DB 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGBALYIGIISLFSLIAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYOAPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYYDAYOAPLATRSSPRPGQPKVKSSEFNSYSLTGYV 230

Search completed: October 27, 2004, 07:17:45  
Job time : 159 secs



Db 121 GGVFFILGLGLGFIPIVAMNHLGILRDYSPPLVDSMKFEIGALYGIISLSFSLAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230  
Db 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230

## RESULT 2

US-10-140-002-492  
Sequence 492, Application US/10140002  
Patent No. 6725730  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C59  
CURRENT APPLICATION NUMBER: US/10/140,002  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 492  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-002-492

Query Match 100.0%; Score 1174; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3e-121;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASLGQLVGYILGLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
Db 1 MASLGQLVGYILGLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPIADIOAAMVTSSAISLACIISVGMKCTVFCQESRAKORVAVA 120  
Db 61 ITQCDIYSTLLGLPIADIOAAMVTSSAISLACIISVGMKCTVFCQESRAKORVAVA 120  
QY 121 GGVFFILGLGLGFIPIVAMNHLGILRDYSPPLVDSMKFEIGALYGIISLSFSLAGII 180  
Db 121 GGVFFILGLGLGFIPIVAMNHLGILRDYSPPLVDSMKFEIGALYGIISLSFSLAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230  
Db 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230

## RESULT 3

US-09-663-600A-92  
Sequence 92, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclet, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 92  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24..-1  
NAME/KEY: UNSURE  
LOCATION: 54,79  
OTHER INFORMATION: Xaa = any one of the twenty amino acids  
US-09-663-600A-92

Query Match 99.0%; Score 1162; DB 4; Length 230;  
Best Local Similarity 99.1%; Pred. No. 6.4e-120;  
Matches 228; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MASLGQLVGYILGLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
Db 1 MASLGQLVGYILGLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPIADIOAAMVTSSAISLACIISVGMKCTVFCQESRAKORVAVA 120  
Db 61 ITQCDIYSTLLGLPIADIOAAMVTSSAISLACIISVGMKCTVFCQESRAKORVAVA 120  
QY 121 GGVFFILGLGLGFIPIVAMNHLGILRDYSPPLVDSMKFEIGALYGIISLSFSLAGII 180  
Db 121 GGVFFILGLGLGFIPIVAMNHLGILRDYSPPLVDSMKFEIGALYGIISLSFSLAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230  
Db 181 LCFSSCSQRNRSNYYDAYOQAPLATRSSPRPGOPPKVKSSEFNSYSLTGYV 230

## RESULT 4

US-09-603-552-13  
Sequence 13, Application US/09603552  
Patent No. 6590089  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Tang, Y. Tom  
APPLICANT: Patterson, Chandra  
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE  
FILE REFERENCE: PC-0016 US  
CURRENT APPLICATION NUMBER: US/09/603,552  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PERL Program  
SEQ ID NO 13  
LENGTH: 220  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Genbank No. 6590089 g2570129







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/ SEQ ID NO 12
/ LENGTH: 211
/ TYPE: PR
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Incycle ID No. 6590089 2057608CD1
US-09-603-552-12

Query Match      34.7%; Score 407.5; DB 4; Length 211;
Best Local Similarity 37.3%; Pred. No. 8.8e-37;
Matches 81; Conservative 41; Mismatches 78; Indels 17; Gaps 2;

QY 1 MASLGLVGVYIIGLGLTLVAMLLPSWKTSSYVGSIVTAVGFSKGLMECATHTSG 60
D 1 MANAGLQLFLFLAFGLMIGAVISTALPQWRIVSYADNIVTQAMVEGLMSCVSGSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGRCVFCQESRA-KDRVAV 119
D 61 QIQCKVDSLNTLSSTLQATRALMVVGILLGVIAIPFATVGMCKMCKLEDDEVQKRMMAV 120
QY 120 AGGVFTLGLGLGIPVAMNHLGRDPSGLVDSKKEFEGALYIGIISLSFLAGI 179
D 121 IGGAIFFLAGLALIVATWAGNRIVQEFYDPMTPVNAFYEGQALFTGMAASICLLIGA 180
QY 180 ILFCSSQRNRSNYDAYQAQPLATRSSPPGQPK 216
D 181 LLCSCC-----PKTTSYTPRPYPK 201

RESULT 10
US-09-886-683A-4
/ Sequence 4; Application US/09886683A
/ Patent No. 6627439
/ GENERAL INFORMATION:
/ APPLICANT: Hoevel, Thorsten
/ APPLICANT: Koch, Stefan
/ APPLICANT: Kubbies, Manfred
/ APPLICANT: Muddisgl, Olaf
/ APPLICANT: Rueger, Petra
/ TITLE OF INVENTION: Antibodies against SEMP1 (p23)
/ FILE REFERENCE: Case 20692
/ CURRENT APPLICATION NUMBER: US/09/886, 683A
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: EP01107799.7
/ PRIOR FILING DATE: 2001-04-05
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 211
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-09-886-683A-4

Query Match      34.7%; Score 407.5; DB 4; Length 211;
Best Local Similarity 37.3%; Pred. No. 8.8e-37;
Matches 81; Conservative 41; Mismatches 78; Indels 17; Gaps 2;
```

```
D 181 LLCSCC-----PKTTSYTPRPYPK 201

RESULT 11
US-09-130-491-14
/ Sequence 14; Application US/09130491
/ Patent No. 6416974
/ GENERAL INFORMATION:
/ APPLICANT: Holtzman, Douglas A.
/ APPLICANT: Goodearl, Andrew D.J.
/ TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
/ FILE REFERENCE: 09404/041001
/ CURRENT APPLICATION NUMBER: US/09/130,491
/ PRIOR FILING DATE: 1998-08-07
/ EARLIER APPLICATION NUMBER: US 60/058,108
/ EARLIER FILING DATE: 1997-09-05
/ EARLIER APPLICATION NUMBER: US 60/054,961
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 218
/ TYPE: PR
/ ORGANISM: Rattus rattus
US-09-130-491-14

Query Match      32.2%; Score 378; DB 4; Length 218;
Best Local Similarity 36.2%; Pred. No. 1.6e-33;
Matches 76; Conservative 52; Mismatches 76; Indels 6; Gaps 3;

QY 1 MASLGLVGVYIIGLGLTLVAMLLPSWKTSSYVGSIVTAVGFSKGLMECATHTSG 60
D 1 MGSALIEILGVLCVGMGLILACGLPMWQVAFPHDNIVTDQTMKGLMNSCVVSGSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACIISVVGRCVFCQESRAKDRVAV 120
D 61 HMCKVDSVLTALSTEVQARALTVAVALFVALFVTLTAGACCTCVAPGPAKAVALT 120
QY 121 GGVFTLGLGLGIPVAMNHLGRDPSGLVDSKKEFEGALYIGIISLSFLAGI 180
D 121 GGVLYLFCGLLAVPLCFWPNIVREFYDPSVPSQTEIGALVYGMATALLMVGGCL 180
QY 181 LC---FSCSSQRNRSNYDAYQA--QPLAT 205
D 181 LCCGANVCTGRPDL--FPVYISAPRRPTAT 209

RESULT 12
US-09-489-847-209
/ Sequence 209; Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ PRIOR FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 209
```

LENGTH: 218  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-489-847-209

Query Match 32.2%; Score 378; DB 4; Length 218;  
Best Local Similarity 36.2%; Pred. No. 1,6e-33;  
Matches 76; Conservative 52; Mismatches 76; Indels 6; Gaps 3;

QY 1 MASLGOLVYILGLIGLITLVAMLLPSKTSYVGAIVTAVGSKGLMCAHSTG 60  
DB 1 MGSALFELGLVCLVGMGGLIACGIPMGTAFEDHNVITVQTTKGLMCCVQSTG 60  
QY 1TTCDDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 120  
DB 61 HMCKKYVSLVSLSTEVQABALTVSAVLAPVALFVTLAQCTTCVAPGAKARVALT 120  
QY 121 GGVFFILGLIGLIPVAMNHLGILRDPYSPVPSDKMFEIGALYIGTISLSLAGII 180  
DB 121 GGVLYLFCGLALVPLCMFANIVREFPVSPVSOKEIGALYIGMATALLMVGGL 180  
QY 181 LC---FSCSGQRNSNYDAYQA--OPLAT 205  
DB 181 LCCGANVCTGRPDL\$-FPVKYSAPRPTAT 209

## RESULT 13

US-09-603-552-1  
Sequence 1, Application US/09603552  
Patent No. 6590089  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: RVP-1 VARIANT DIFFERENTIALLY EXPRESSED IN CROHN'S DISEASE  
FILE REFERENCE: PC-0016 US  
CURRENT APPLICATION NUMBER: US/09/603,552  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PERL Program  
SEQ ID NO 1  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6590089 1456746CD1  
US-09-603-552-1

Query Match 26.8%; Score 314.5; DB 4; Length 228;  
Best Local Similarity 32.5%; Pred. No. 1.8e-26;  
Matches 78; Conservative 47; Mismatches 90; Indels 25; Gaps 10;

QY 3 SLGLQVGYILGLIGLITLVAMLLPS--WKTSSYVGAIVTAVGSKGLMCAHSTG 60  
DB 2 SMAVEFFGFMAVVGGL--MLGVTLPPSYVRVST-VHGNVITNTJTFENLWFCADSLG 58  
QY 1TTCDDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 120  
DB 59 VYMCWEPSPMLALSGYQACRALMTIALLGLLGLIGLIGLACTN--GGLSKRYQA 116  
QY 121 GG---VFFILGLIGLIPVAMNHLGILRDPYSPVPSDKMFEIGALYIGTISLSLAGII 177  
DB 117 GGRRALHIIAGICGWAIAISWYAFNITRDFPDLPYGT-KYELGPAIYLTMSASLSILG 175  
QY 178 GILLCBSC---SSGRKSNYDAYQA---QPLATRSPPRGQPKKSEFNYSILGYV 230  
DB 176 GLCLCSACCGSDPDPASARRPYQAEVSVMPVAT--SDQEGD-----SSFGRYGRNAVY 228

RESULT 14  
US-09-724-864-64  
Sequence 64, Application US/09724864

Patent No. 6380362  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
FILE REFERENCE: 11000.1050U1  
CURRENT APPLICATION NUMBER: US/09/724,864  
CURRENT FILING DATE: 2000-11-28  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Mouse  
US-09-724-864-64

Query Match 23.4%; Score 275; DB 3; Length 264;  
Best Local Similarity 27.3%; Pred. No. 4.9e-22;  
Matches 62; Conservative 48; Mismatches 101; Indels 16; Gaps 4;

QY 1 MASLGOLVYILGLIGLITLVAMLLPSKTSYVGAIVTAVGSKGLMCAHSTG 60  
DB 1 MATTCQVVGVLISLGLAGCIAAGMDMNSTQDLYD-NPVTAVFQHGLMRSVQOQSSG 59  
QY 61 ITTCDDIYTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAV 119  
DB 60 FTBCREYFTIILGIPALQVRAIMVIGYIGLIVSIFALKICIRIGMDSAKAKMTL 119  
QY 120 AGGVFFILGLIGLIPVA-----W-----NLHGLRDPYSPVPSDKMFEIGALY 165  
DB 120 TSGILFELIGICAIIGSVFANMLVTNFMWSTANMYSGMGKGVQVQTRVFGALF 179  
QY 166 LGIISLPSLIGIILCFSCSGQRNSNYDAYQAOPLATRSPPRG 212  
DB 180 VGVNAGGLTLIGVMMCIACRGTLTPDPSNFKAVSTHASQNAVYRPG 226

## RESULT 15

US-09-188-930-174  
Sequence 174, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188,930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 174  
LENGTH: 137  
TYPE: PRT  
ORGANISM: Human  
US-09-188-930-174

Query Match 19.0%; Score 223.5; DB 3; Length 137;  
Best Local Similarity 35.7%; Pred. No. 9.1e-17;  
Matches 41; Conservative 30; Mismatches 43; Indels 1; Gaps 1;

QY 67 YSTLGLPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVAGGVFF 125  
DB 7 YDSVIALSAALQTRALMVVSLVIGLAFAMFVATMGKCTRCGGDDRVKARIAMGGIIF 66  
QY 126 ILGLIGLIPVAMNHLGILRDPYSPVPSDKMFEIGALYIGTISLSLAGII 180

Db 67 IVAGLAALVACSWYGHQIVTDFYNP LIPTNIKYEPGPAIFIGWAGSALVILGGAL 121

Search completed: October 27, 2004, 07:22:34  
Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:11:11 ; Search time 38 Seconds  
(without alignments)  
582.365 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 1174  
Sequence: 1 MASLGLVGVYILGLGLG.....PGQPKVKSSEFNSYLTGVY 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_79:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*  
5: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	423.5	36.1	280	A39484	androgen-withdrawn
2	100	8.5	400	AG2866	MPS permease [drug]
3	100	8.5	400	D97643	probable efflux pr
4	99.5	8.5	330	C69648	2-keto-3-deoxygluc
5	99.5	8.5	463	F90285	metabolite transpo
6	97.5	8.1	484	C75609	amino acid ABC tra
7	95.5	8.1	458	H71657	NADH2 dehydrogenas
8	93	7.9	523	T11916	NADH2 dehydrogenas
9	91	7.8	160	TJ1916	peripheral myelin
10	90.5	7.7	487	TJ19237	hypothetical prote
11	90.5	7.7	429	A71019	hypothetical prote
12	88.5	7.5	617	A97241	permease [imported
13	88.5	7.5	521	A99549	amino acid permeas
14	88.5	7.5	593	H71283	conserved hypothet
15	88	7.5	160	A41144	growth arrest-tela
16	88	7.5	421	A99309	membrane transport
17	88	7.5	906	G90281	conserved hypothet
18	87.5	7.5	268	A71086	hypothetical prote
19	87.5	7.5	420	H96534	probable Na+/H+ an
20	87.5	7.5	519	T15364	hypothetical prote
21	87.5	7.5	690	S35251	tumor-associated m
22	87	7.4	157	G02355	probable membrane
23	87	7.4	160	S21721	growth arrest-spec
24	87	7.4	223	B87654	hypothetical prote
25	87	7.4	318	AG3576	iron(III) dicitrat
26	87	7.4	414	B85970	probable transport
27	87	7.4	414	F65097	hypothetical 43.5
28	87	7.4	414	C91125	probable transport
29	86.5	7.4	255	B64604	conserved hypothet

30	86.5	7.4	402	A11853	sodium-dependent n
31	86.5	7.4	432	A70714	hypothetical prote
32	86.5	7.4	428	D97799	NADH2 dehydrogenas
33	86.5	7.4	497	AD3525	amino acid permeas
34	86.5	7.4	547	B64963	membrane protein y
35	86	7.3	388	UQ0113	2-keto-3-deoxygluc
36	86	7.3	409	S29124	membrane glycoprot
37	86	7.3	552	T52481	cytochrome-c oxida
38	85.5	7.3	216	I38474	olfactory receptor
39	85.5	7.3	371	D75266	cell division prot
40	85.5	7.3	414	AG0894	probable membrane
41	85.5	7.3	445	T11097	NADH2 dehydrogenas
42	85	7.2	233	T31865	hypothetical prote
43	85	7.2	502	B70845	probable sugar tra
44	85	7.2	531	T11074	NADH2 dehydrogenas
45	84.5	7.2	454	C86766	hypothetical prote

## ALIGNMENTS

## RESULT 1

A39484 androgen-withdrawal apoptosis protein RVPI, prostatic - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 04-Mar-2000

C/Accession: A39484

R/Briehl, M.M.; Miesfeld, R.L.

Mol. Endocrinol. 5, 1381-1388, 1991

A/Title: Isolation and characterization of transcripts induced by androgen withdrawal and

A/Reference number: A39484; MUID:92130987; PMID:1723140

A/Accession: A39484

A/Molecule type: mRNA

A/Residues: 1-280 <BRI>

A/Cross-references: GB:W4067; NID:G205857; PIDN:AAA41760.1; PID:G205858

C/Genetics:

A/Gene: RVP.1

C/Superfamily: rat androgen-withdrawal apoptosis protein RVPI

Query Match	36.1%;	Score 423.5;	DB 2;	Length 280;
Best Local Similarity	37.7%;	Pred. No. 2.4e-28;		
Matches	84;	Conservative 50;	Mismatches 74;	Gaps 3;
Qy	3	SLGLVGVYILGLGLGTVAMLLPSMKTSSVYGASIVTAVGFSKLGMECAHSTGIR	62	
Db	2	SMSLIRGTSLAVGLMCTIVCCALPMKRVSAFSGSIITHTQTBEGLMNC-VQSTGQM	60	
Qy	63	QCDIYSTLGLPADIQAAQAMVYTSSAISLACTISVGMRCVFCQESRAKDRVAVAGG	122	
Db	61	QCKRYDSLLALPDQLQARALIVSILAAFGLLVLAQVGAQNCNVQDFAKAKITIVAG	120	
Qy	123	VPTLGLGLFIPYANMHLGILDFSPVLPDMSKPFEGALVIGTISLSFLIAGIILC	182	
Db	121	VLFLAAVLTLPVPSWANTIRDFYNPVPEAQKREMGGLVGMMAAQLQLGALLC	180	
Qy	183	FSCSSORNSRNYDAYOAPLAT-----RSSPRPG	212	
Db	181	CSCPPREKRYPTKILYSA-PRSTGPGTGTATDRKTTSRPG	222	

## RESULT 2

AG2866 MPS permease [drug] [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C/Accession: AG2866

R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCellie

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AG2866  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <KUR>  
A:Cross-references: UNIPROT:Q8UCX2; GB:AE008688; P1DN:AA143349.1; P1D:G17740844; GSPDB:C  
A:Experimental source: strain C58 (Dupont)  
A:Gene: Atuz361  
A:Map position: circular chromosome

Query Match 8.5%; Score 100; DB 2; Length 400;  
Best Local Similarity 21.2%; Pred. No. 0.56;  
Matches 44; Conservative 31; Mismatches 67; Indels 66; Gaps 7;

QY 8 LVGYILGLGLTIVAMLLPSWKTSSYVGSIVTAVGFGKLMMECATSTGTGCDIY 67  
DB 243 VAGYATIGFNLGALMA--LSFGRLRIRIGVTYLLAGL-----VLMATG----- 286  
QY 68 STLGLPADIOAQMAMVTSASISLACTISVVG-----MRTVFCQESRAKDRY 117  
DB 287 -----ALATAGGLSSMLALAVGAGVAMPISMTTLMALPLRLRGRI 332  
QY 118 A--VAGGFPIGLGLGFIIVANMLHGLIDFYSPLVPDSMKKEIGALYIGIISLFSL 175  
DB 333 AGIVTASMF-----LGHFISPLVSQPMIARFGPATYTRDIALVFAV 373  
QY 176 IAGIILCFSCSSQGRNSNYDAYOAPL 203  
DB 374 MAGLAIAITIFORT-----GIRKQPL 396

RESULT 3  
D97643  
probable efflux protein cjl687 (imported) - Agrobacterium tumefaciens (strain C58, Cerec  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: D97643  
R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurolo, B.; Goldman,  
A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: D97643  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <KUR>  
A:Cross-references: UNIPROT:Q8UCX2; GB:AE007869; P1DN:AAK8101.1; P1D:G15157533; GSPDB:C  
A:Gene: AGR\_C\_4286  
A:Map position: circular chromosome

Query Match 8.5%; Score 100; DB 2; Length 400;  
Best Local Similarity 21.2%; Pred. No. 0.56;  
Matches 44; Conservative 31; Mismatches 67; Indels 66; Gaps 7;

QY 8 LVGYILGLGLTIVAMLLPSWKTSSYVGSIVTAVGFGKLMMECATSTGTGCDIY 67  
DB 243 VAGYATIGFNLGALMA--LSFGRLRIRIGVTYLLAGL-----VLMATG----- 286  
QY 68 STLGLPADIOAQMAMVTSASISLACTISVVG-----MRTVFCQESRAKDRY 117  
DB 287 -----ALATAGGLSSMLALAVGAGVAMPISMTTLMALPLRLRGRI 332  
QY 118 A--VAGGFPIGLGLGFIIVANMLHGLIDFYSPLVPDSMKKEIGALYIGIISLFSL 175  
DB 333 AGIVTASMF-----LGHFISPLVSQPMIARFGPATYTRDIALVFAV 373  
QY 176 IAGIILCFSCSSQGRNSNYDAYOAPL 203  
DB 374 MAGLAIAITIFORT-----GIRKQPL 396

RESULT 4  
C69648  
2-Keto-3-deoxygluconate permease kdgT - Bacillus subtilis  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: C69648  
R/Kunst, F.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec  
C./Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Eutim, K.D.; Erlington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gallie  
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lepidus, A.; Lardinois,  
A.; Authors: Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Meisel,  
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,  
A.; Authors: Tanaka, A.; Tanaka, T.; Tespstra, P.; Tognoni, A.; Tostato, V.; Uchiyama, K.  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: C69648

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-330 <KUN>  
A:Cross-references: UNIPROT:P50847; GB:Z99115; GB:AL009126; NID:G2634478; P1DN:CAB14126.J  
A:Experimental source: strain 168  
A:Gene: kdgT

Query Match 8.5%; Score 99.5; DB 2; Length 330;  
Best Local Similarity 24.4%; Pred. No. 0.51;  
Matches 51; Conservative 30; Mismatches 77; Indels 51; Gaps 11;

QY 2 ASIGLQVGYI-----LGLGLGLTIVAMLLP--SWKTSSYVGSIVTAVGFG-- 46  
DB 60 ATIDFSSSGYIARKGTTLLGKIGFALGIVNAQPIPDGIGSGFAGISVATVAVNM 119  
QY 47 --SKGLMECATSTGTGCDIYVTLGLPADIOAQMAMVTSASISLACTISVGMRC 104  
DB 120 ETMGGLYALMNR-----MGRKED--AGAFAPISTSGPFMTVTGCVGL-- 163  
QY 105 TVFCQESRAKDRVAVAGVFFILGLGFIIVANMLHGLIDFYSPLVP--DSMKKEIG 161  
DB 164 AAFPMTETLA-----ATVIFPIGLGILG-----NDDHDLRDFSKVPAIIPFPAFSLG 211  
QY 162 EALYVIGII--SLSFLIAGI--ILCFSCSS 167  
DB 212 NTLNFGMLIQSGLGIFIGSVVILSGSS 240

RESULT 5  
F90285  
metabolite transport related protein SSO1305 (imported) - Sulfolobus solfataricus  
C/Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: F90285  
R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
submitted to Genbank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: F90285  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-463 <KUR>  
A:Cross-references: UNIPROT:Q97YU8; GB:AE006641; NID:G13814507; P1DN:AAK41541.1; GSPDB:G  
A:Gene: SSO1305

Query Match 8.5%; Score 99.5; DB 2; Length 463;



Best Local Similarity 23.8%; Pred. No. 0.71;  
Matches 44; Conservative 35; Mismatches 59; Indels 47; Gaps 10;  
QY 6 LQVYIIGLGLTIVAMLLPSWKTSYVGSIVTAVGSGKLMW 56  
DB 288 VQIAFPVTAITGVVGMQSDKVRNRLVAVSSLCIAIGPILGPFILVWALFNVF 347  
QY 57 -----HSTGI-TCDDIYTLGLPADIQ-AAQ-----AMVTSSAISLACTISV 100  
DB 348 LPEFGHMLMPQTRVSTEL-PTEIRNTRAGVGMWGMIALGINSIFVPS---ITTVI 403  
QY 101 GMRCTVFCQESRAKRVAVAGVFFIIGLGFIPVAMNLHG-----ILDFYSPVLPDS 155  
DB 404 GY-----SAIAAVATSPFIIITIGLL-VGPDRHGSLEIVINDFYGKVPVS 450  
QY 156 MKFEI 160  
DB 451 KVEV 455  
RESULT 6  
C75609  
amino acid ABC transporter, permease protein - Deinococcus radiodurans (strain R1)  
C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: C75609  
R/White, O.; Eiken, J.A.; Heideberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venner, J.C.; Fraser, C.M.  
S/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266  
A/Accession: C75609  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-484 <WHI>  
A/Cross-references: UNIPROT:Q9R217; GB:AE001862; GB:AE001825; NID:G6460468; PIDN:AAF1222  
A/Experimental source: strain R1  
C/Genetics:  
A/Genes: DRA0136  
A/Map position: 2  
Query Match 8.3%; Score 97.5; DB 2; Length 484;  
Best Local Similarity 26.1%; Pred. No. 1.1;  
Matches 55; Conservative 25; Mismatches 84; Indels 47; Gaps 9;  
QY 14 GLLGLTIVAMLLPSWKTSYVGSIVTAVGSGKLMWCAHSTGITOCDIYTLGL 73  
DB 164 GVAGALAFVAVPPLGKNTIGLVQYRNVADTF---WPQIGTHAALSVIALALLGL 219  
QY 74 PAIQAAQAMMTSSAL---SSLACTISV---GMRCTVFCQESRAK----- 115  
DB 220 PLGIAAARNRTRLAGVGFASFLQITIPSVALLFGLLPVFSALGVSAGVAFPLANSALL 279  
QY 116 -----RVAVAGVFFIIG-----GLLGFIPVAM-NLHGILDFYS---PLV 152  
DB 280 LGIALTRVRLALPGLLALGQALLAGLGLVQLQGMFGSDLSRDPASLSAPLA 339  
QY 153 PDSMKFEIGALYGIISLPSLIAGITLCP 183  
DB 340 SMGVR-GIGAAPALFAL-TLYALLPIVNTF 368  
RESULT 7  
H71657  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain N RP537 - Rickettsia prowazekii  
C/Species: Rickettsia prowazekii  
C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C/Accession: H71657  
R/Anderson, S.G.B.; Zomorodipour, A.; Anderson, J.O.; Sichteritz-Ponten, T.; Almark, U  
Nature 396, 133-140, 1998  
S/Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A/Reference number: A71630; MUID:39039499; PMID:9823893

A/Accession: H71657  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-458 <AND>  
A/Cross-references: UNIPROT:Q9ZD13; GB:AJ235272; GB:AJ235269; NID:G3861033; PIDN:CAA14986  
A/Experimental source: strain Madrid B  
C/Genetics:  
A/Genes: nuon1, RP537  
A/Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
C/Keywords: membrane-associated complex; NAD; oxidoreductase  
Query Match 8.1%; Score 95.5; DB 2; Length 458;  
Best Local Similarity 23.6%; Pred. No. 1.5;  
Matches 59; Conservative 33; Mismatches 73; Indels 85; Gaps 12;  
QY 13 LGLGLTIVAMLLP-----SWKTSYVGSIVTAVGSGKLMW 52  
DB 10 LTLIALGQCFALMIDNKRRIYIVILCTISIFLTFKSYI-----EGIWH 57  
QY 53 ECAT-HSTGITQCDI-----YSTLLGLPADIQAAQAMMT-----SSAISLA 94  
DB 58 SPATERNIGISKIILLFTVSLIYRDYSILVGERLKEFTLMLSIVGIFVALISRN 117  
QY 95 CIISVGMRCVFCQESRA---KDRVAVAGV-FTIIGLGFIPVAMNLHG----- 143  
DB 118 FLLPGCMELTALTSYALAGFKLNDIKSEGALKYFILLSIVSCL---SLFGISFIYGP 173  
QY 144 -----ILDFYSPVPPSMKFEIGALYGI---SSLFSLINAGIILCFSCSSGRNSNY 195  
DB 174 GSGIQFDILHQNDS---EIKPGLIGIVLFSLSIFFKLASSPLHFIP----- 221  
QY 196 DAYAQOPLAT 205  
DB 222 DYEKSPIS 231  
RESULT 8  
T11916  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Prototheca wickerhamii mitochondrion  
C/Species: mitochondrion Prototheca wickerhamii  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T11916  
R/Molff, G.; Planke, I.; Lang, B.F.; Kueck, U.; Burger, G.  
J. Mol. Biol. 237, 75-86, 1994  
S/Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca w.  
A/Reference number: Z17373; MUID:94180393; PMID:8133522  
A/Accession: T11916  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-523 <MOL>  
A/Cross-references: UNIPROT:Q37617; EMBL:U02970; NID:G467843; PIDN:AAJ12635  
A/Experimental source: strain HB-8  
C/Genetics:  
A/Genome: mitochondrion  
A/Note: nad4  
A/Superfamily: NADH dehydrogenase (ubiquinone) chain 4  
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;  
Query Match 7.9%; Score 93; DB 2; Length 523;  
Best Local Similarity 24.2%; Pred. No. 2.8;  
Matches 45; Conservative 37; Mismatches 50; Indels 54; Gaps 11;  
QY 8 LVGYIIGLGL-LLGLTIVAMLLPSWKTSY---VGASIVTAVGSGKLMWCAHST-- 59  
DB 24 IMGYIEMVTAIPPLGIALLEVPSWKTYQTRINALNSSLTFL-LSLLWTFPDSALP 82  
QY 60 -----GITQCDIYTLGLPADIQAAQAMMTSSAISLACTISVGMRCVFCQESRAKD 115  
DB 83 QPFDGVSPIVVS-----DVTLAKA--ASSSFPALNALGVDI----- 120  
QY 116 RVAVAGVFFIIGLGFIP---VAM-NLHGILDFYSPVDSMKFEIGALYGIIS 170  
DB 121 -----SLPFIILITTL-LVPICTIVSWNNIEVVKEY-----CIAFVLTLTMTLVS 166

Qy	171	SLFSLI	176
		:	
Db	167	VLDLLI	172

	RESULT	9
TNOE03		

peripheral myelin protein 22 - human  
N/Alternate names: Charcot-Marie-Tooth, GMS-3 protein; growth arrest-specific protein 3  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: JN0503, JCI190, A56697, S25537  
R/Edom, P.; Martiniotti, A.; Colombo, M.P.; Schneider, C.  
Gene 126, 289-290, 1993  
A/Title: Sequence number of human GMS3/PMP22 full-length cDNA.  
A/Reference number: JN0503; MUID:93246261; PMID:8482547  
A/Accession: JN0503  
A/Molecule type: mRNA  
A/Residues: 1-160 <EDO>  
A/Cross-references: UNIPROT:Q01453; GB:L03203; NID:g182984; PIDN:AA58495.1; PID:g182985  
R/Hayaaka, K.; Himoto, M.; Nanao, K.; Sato, W.; Mura, M.; Uyemura, K.; Takahashi, E.;  
Biochem. Biophys. Res. Commun. 186, 827-831, 1992  
A/Title: Isolation and sequence determination of cDNA encoding PMP-22 (PAs-II/SR3/GMS-3)  
A/Reference number: JCI190; MUID:92360032; PMID:1497668  
A/Accession: JCI190  
A/Molecule type: mRNA  
A/Residues: 1-160 <GB>  
A/Cross-references: GB:D11428; NID:g220009; PIDN:BAA01995.1; PID:g220010  
R/Valentini, L.J.; Baas, F.; Wolterman, R.A.; Hoogendijk, J.E.; van den Bosch, N.H.A.; Z  
Nature Genet. 2, 288-291, 1992  
A/Title: Identical point mutations of PMP-22 in Trembler-J mouse and Charcot-Marie-Tooth  
A/Reference number: A56697; MUID:93265161; PMID:1303281  
A/Accession: A56697  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-160 <VAL>  
A/Cross-references: GB:661788  
R/Colombo, M.  
Submitted to the EMBL Data Library, May 1992  
A/Reference number: S25537  
A/Accession: S25537  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 61-160 <COL>  
A/Cross-references: EMBL:X65968; NID:g31652; PIDN:CAA6781.1; PID:g31653  
C/Genetics:  
A/Genes: GDB:PMP22; GMS3  
A/Cross-references: GDB:134190  
A/Map position: 17p12-17p11.2  
C/Superfamily: growth arrest-specific protein  
C/Keywords: myelin; transmembrane protein

Query Match	7.8%;	Score 91;	DB 2;	Length 160;
Best Local Similarity	21.7%;	Pred. No. 1.3;		
Matches 41;	Conservative 33;	Mismatches 69;	Indels 46;	Gaps 8

```

QY      1 M A S I G L Q V Y I L G I L G I L G I T V A M L L P B K R T S S Y V G A S Y T A N G F S K G L M E A T S T G 60
Db      1 M L L L L S I T V L A H A V L V L L - F V S T T S Q W ----- I V G N G H A T D L M Q N C S T S S G 48

QY      61 I T O C D I Y S T L L G L P A D - I Q A Q M A M V T S G A I S L A C I I S V G M E C T V F C E S R A K D H V A V 119
Db      49 - - - - N V H C H S S E N M E L O S V Q A T M L S I T F S - - - - I L S L P F C Q L F T L T K G R F I T - 99

QY      120 A G S V P F I L G G L G F I V A - - - - - A N L I G L R D F S P L V P D S K E I G E A L Y L G I I S S 171
Db      100 - - G I F O I L G L C M S P A A I Y T V R B P H M I N S - - - - - D Y S Y G A Y I L A W A F 143

QY      172 L P S L I N G I I 180
Db      144 P L A L L S G V I 152

```

**RESULT 10**

hypothetical protein C27A7.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T19237, T19502  
R:Haris, B.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z15095  
A:Accession: T19237  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-487 <WIL>  
A:Cross-references: UNIPROT:O01932, EMBL:Z52825, PIDN:CAB07317.1, GSPDB:GN00023, CESP:C27A7.6  
A:Experimental source: clone C13C4  
R:Haris, B.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19132  
A:Accession: T19502  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-487 <WIL>  
A:Cross-references: EMBL:Z61041, PIDN:CAB02792.1, GSPDB:GN00023, CESP:C27A7.6  
A:Experimental source: clone C27A7  
C:Genetics:  
A:Gene: CESP:C27A7.6  
A:Map position: 5  
A:Intons: 30/3, 51/3, 87/3, 109/3, 183/1, 215/3, 264/2, 302/2, 330/3, 349/3, 372/1, 433/1

Query Match	7.7%;	Score 90.5;	DB 2;	length 487;
Best Local Similarity	28.7%;	Pred. No. 4.3;		
Matches 51;	Conservative 17;	Mismatches 79;	Indels 31;	Gaps 7,

QY 5 GQGLVYIIIGLGLIGLGTVMALLP--SKRTSSVYGA\$IVTVAGSGK---LMECAHST 59  
D 297 GEMMAYPAVCAVIGTLLSLAGHIAKTRKFEIINVCVSGSCSYIITRMPLNPRT 35  
QY 60 GINQCDIVSTLLGLPADIGAAQAMWVTSSAISLACISY-VGRKCTVFCQ\$BAKQVA 118  
D 297 GEMMAYPAVCAVIGTLLSLAGHIAKTRKFEIINVCVSGSCSYIITRMPLNPRT 35  
QY 357 GLPDSIIIVTLTG-----CIGANSIPQPIGVGLGVETTFPPVME-----A 396  
D 357 GLPDSIIIVTLTG-----CIGANSIPQPIGVGLGVETTFPPVME-----A 396  
QY 119 VAGGVFFIIGGLGF-IPVAMNHLGLDRPVSPLVDSMKFEIGALYLGIISLSF\$ 175  
D 397 TSSGVLIVTGS\$LFMTIIPPAQNTYKHLFIA---Q\$WKALDVTGSLIVSYIISL 450

## RESULT 11

hypothetical protein PH1451 - *Pyrococcus horikoshii*  
C/Species: *Pyrococcus horikoshii*  
C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #next\_change 12-Jul-2004  
C/Accession: F71019  
R/Kawarabayashi, Y., Sawada, M., Horikawa, H., Halkawa, Y., Hiro, Y., Yamamoto, S., Sekine, M., Ohtsuka, Y., Funahashi, T., Tanaka, T., Kodon, Y., Yamazaki, J., Kuehida, N., Oguchi, D. N. A. Rev. 5, 55-76, 1998  
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon  
A/Reference number: A71000; NCBI:98344137; PMID:9679194  
A/Accession: F71019  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-617 <RAW>  
A/Cross-references: UNIPROT:O59120; GB:AP000006; NID:G3336133; PIDN:BA30558.1; PID:G325  
A/Experimental source: strain OT3  
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C/Genetics:  
C/Gene: PH1451

Query Match	7.7%;	Score 90.5;	DB 2;	Length 617;
Best Local Similarity	24.4%;	Pred. No. 5.4;		
Matches 52;	Conservative 33;	Mismatches 81;	Indels 47;	Gaps 9

Qy 5 GLQLVGYILGLL-----GLVAMLLPSMKTSSY-----VGASIVTAVGFS-- 47  
 Db 273 GTPLFGITIAFLGLLITIGGLVLAALQEDIRKLFVASSISQVGYILVGLIGISLGEAA 332  
 Qy 48 -----KGL-WMECAT--HSTGITQCDISTLLGLPADIOAQAAMVTS-----AI 90  
 Db 333 IYNAISHALPKFGFLVAVATITVYRTGKTEFDFGGL-----AKMPTFMARFIAI 383  
 Qy 91 SSIACTISVGMCTVCGSRAKDRVAVAGVFFILGLLGFIPVAMNHLGRDYSF 150  
 Db 384 LSLAGLPPLVFPASKWILFRAVISQKPLILGMLF-PGSAIGFVYLIRFTYAVFGGRPS 442  
 Qy 151 LVPSDMKEIGALYGLISL--FSLIAGII 180  
 Db 443 DIEDTKDAPLPLAIGMILGLTANVFGVAPGLV 475

## RESULT 12

A97241  
 permease (imported) - Clostridium acetobutylicum  
 C/Species: Clostridium acetobutylicum  
 C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C/Accession: A97241  
 R;Molling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
 A;Reference number: A96900; MUID:21359325; PMID:21359325  
 A;Accession: A97241  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-429 <KUR>  
 A;Cross-references: UNIPROT:Q97FG7; GB:AE001437; PIDN:AAK80716.1; PID:915025810; GSPDB:C  
 A;Experimental source: Clostridium acetobutylicum ATCC824  
 C/Genetics:  
 A;Gene: CAC2772  
 C;Superfamily: conserved hypothetical protein H1025

Query Match 7.5%; Score 88.5; DB 2; Length 429;  
 Best Local Similarity 22.8%; Pred. No. 5.6;  
 Matches 41; Conservative 38; Mismatches 76; Indels 25; Gaps 8;

Qy 13 LGLLGLLG-FLVAMLLPSMKTSSYVGASIVTAVG-----SKGLWMECATH-----S 58  
 Db 79 MGLNALFTYITICIGLHSMKTA--LALSILGIFVLVLPKIRQLILDSVPQTLKTAIS 136  
 Qy 59 TGITQCDISTLLGL--PADIOAQAAMVTSAISLACTISVGMCTVCGSRAKDR 116  
 Db 137 IGI---GFITPILGLQAGIIVGSKGLTVLASKSPAVILAVILLINLVKNIKGS 193  
 Qy 117 VAVAGVFFILGLLGFIPVAMNHLGRDYSFPLVPSDMKEIGALYGLISLFLSI 176  
 Db 194 FVIGMLVIVYGLIFG--VAKAPSGIV-SPPSVAVPFLQDFKSAVIVGIVEVILTML 249

## RESULT 13

A99549  
 amino acid permease (imported) - Mycoplasma pulmonis (strain UAB CTIP)  
 C/Species: Mycoplasma pulmonis  
 C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C/Accession: A99549  
 R;Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;  
 Nucleic Acids Res. 29, 2145-2153, 2001  
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
 A;Reference number: A99512; MUID:21267165; PMID:11353084  
 A;Accession: A99549  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-521 <KUR>  
 A;Cross-references: UNIPROT:Q96OR4; GB:AI445566; PID:914089711; PIDN:CAIC13470.1; GSPDB:C  
 A;Experimental source: strain UAB CTIP  
 C/Genetics:  
 A;Gene: MYPu\_2970

A;Genetic code: SGC3

Query Match 7.5%; Score 88.5; DB 2; Length 521;  
 Best Local Similarity 21.2%; Pred. No. 6.7;  
 Matches 50; Conservative 38; Mismatches 63; Indels 85; Gaps 11;

Qy 1 MASLGLVGYILGLLGLTIVAMLL-----PSWKTSSYVGA--SIVTA 43  
 Db 1 MSEKTRKXGFFALMLNLGSSVVGIGIFPKNGSVRAVEHNGTSMILAWFGGII SLAA 60  
 Qy 44 VGRSK-----GLWMECATSTG-----ITQCDISTLLG----- 72  
 Db 61 INFSEISFLNKTIXIAGNW---SHKVGDKRGEVVISFTLFGYGIQIILGFTAEI 116  
 Qy 73 -----LPADIOAQA--AMVTSAISLACTISVGMCTVCGSRAKDRVAVAGV 124  
 Db 117 FPHMLNLGANNIMKEMHSLVGLTIVISFTIINIVSIK-----ASGVF 160  
 Qy 125 FILGLLGFIP-VAMNHLGI-----LRDYSPLVPSDMKEIGALYGLISL 172  
 Db 161 QVITTIKKPLPLATILVGLIFVSTHTLEDGANAAPVFNKTK-KIGFSFANVIAL 215

## RESULT 14

H71283  
 conserved hypothetical integral membrane protein TP0771 - syphilis spirochete  
 C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: H71283  
 R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo  
 rthy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-389, 1998  
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
 A;Reference number: A71250; MUID:98332770; PMID:9665876  
 A;Accession: H71283  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-593 <COL>  
 A;Cross-references: UNIPROT:O83750; GB:AE001248; GB:AE000520; NID:93323074; PIDN:JAC6573;  
 A;Experimental source: strain Nichols  
 C/Genetics:  
 A;Gene: TP0771

Query Match 7.5%; Score 88.5; DB 2; Length 593;  
 Best Local Similarity 23.2%; Pred. No. 7.7;  
 Matches 45; Conservative 36; Mismatches 72; Indels 41; Gaps 8;

Qy 4 LGLVGYILGL-----LGLLGLTIVAMLLPSMKTSSYV-----GASIVTAVGFSKGLWMEC 54  
 Db 177 LGSIMGF--GLLFTGLLSSILPPL--SVEELSFLKTAVERALSVPFGLLSFVLTV 232  
 Qy 55 ATHSTGITQCDISTLLGLPADIOAQAAMVTSAISLACTISVGMCTVCGSRAK 114  
 Db 233 ILHSSATTAIVLTMAFGVIGVFAAASVIGSNVSTDAIAAIG-----SKLN 283  
 Qy 115 DRVAVAGVFFILGLLGFIPVAMNHLGRDYSF-----LVPSDMKEIGALYGL 167  
 Db 284 ARRAAAVHVLFFNFGALVFLM-----FFHPLALLCVLTPLNNGFD-NITVRLA 331  
 Qy 168 IISLFLGLIITL 181  
 Db 332 LFHSMFIVIVTIV 345

## RESULT 15

A41144  
 growth arrest-related myelin protein precursor, sciatic nerve - rat  
 N/Alternate names: Schwann cell membrane glycoprotein, SNG  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: A41144; S18550; A44826  
 R;Welcher, A.A.; Suter, U.; De Leon, M.; Snipes, G.J.; Shooter, E.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 7195-7199, 1991  
A/Title: A myelin protein is encoded by the homologue of a growth arrest-specific gene.  
A/Reference number: A41144; MUID:91334432; PMID:1714591  
A/Accession: A41144  
A/Molecule type: mRNA  
A/Residues: 1-160 <MBL>  
A/Cross-references: UNIPROT:P25094; GB:M69139; NID:G207063; PIDN:AAA73063.1; PID:G207064  
R/Spreyer, P.; Kuhn, G.; Hanemann, C.O.; Gyllen, C.; Schaal, H.; Kuhn, R.; Lemke, G.; Mu  
EMBO J. 10, 3661-3668, 1991  
A/Title: Axon-regulated expression of a Schwann cell transcript that is homologous to a  
A/Reference number: S18550; MUID:92037527; PMID:1935894  
A/Accession: S18550  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-29, 'E', 31-160 <SPR>  
A/Cross-references: EMBL:X62431; NID:G55903; PIDN:CAA44297.1; PID:G55904  
R/Heperink, M.E.; O'Neill, A.; Magnoni, G.; Kollmann, R.L.; Heinrichson, R.L.; Zucher-N  
J. Neurosci. 12, 2177-2185, 1992  
A/Title: SAG: a Schwann cell membrane glycoprotein.  
A/Reference number: A44826; MUID:92300442; PMID:1376775  
A/Accession: A44826  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-21, 'K', 23-25, 'K', 27, 'R', 29-30 <DIE>  
A/Note: Sequence extracted from NCBI backbone (NCBI:106581)  
C/Comment: The predicted signal sequence may not be cleaved in some cell types.  
C/Superfamily: growth arrest-specific protein  
C/Keywords: glycoprotein; Schwann cell; transmembrane protein

Query Match 7.58; Score 88; DB 2; Length 160;  
Best Local Similarity 25.88; Pred. No. 2.3;  
Matches 46; Conservative 26; Mismatches 70; Indels 36; Gaps 8;

QY 12 ILGLGLGLVLMLEPSMTSSVGSIVTAVGFSKGLMMECATSTGTCDDYSTLL 71  
Db 2 LELLLGLFLHIVLVLP-VSTIVSQMLV-GNGHRTDLMQNTTSMAGAVQ-HCYSS-- 56  
QY 72 GLPADIQAAQAMVVTSSAISLACISVGMRCIVFCQ-ESRAKDRVAVAGVFFILGGL 130  
Db 57 SVSEMWLQSVQATWILSVTFVLSLFL-----FFCQLFTLTKGGRFYITGVFQILAGL 108  
QY 131 LGFTIPVA-----WNHGLINDFYSPLVPDSMKFEIGALYIGIISLPSLIAGIT 180  
Db 109 CWSAAAIYTVRHSSEWVNN-----DYSYGFAYILAWVAFPLALISGII 152

Search completed: October 27, 2004, 07:21:49  
Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: October 27, 2004, 06:56:41 ; Search time 196 Seconds  
(without alignments)

675.185 Million cell updates/sec

Title: US-09-787-677a-3

Perfect score: 1174  
Sequence: 1 MASIGLQVGVIGLGLG.....PGQPKVKSEFNSYLGYV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	230	1 CLD2_HUMAN	P57739 homo sapien
2	1174	100.0	230	2 BAC11575	Bac11575 homo sapi
3	1174	100.0	230	2 AAH71747	Aah71747 homo sapi
4	1119	95.3	230	1 CLD4_CANFA	Q95K66 canis fami
5	1114	94.9	230	2 Q765F1	Q765F1 bos tauru
6	1114	94.9	230	2 BAD01111	Bad01111 bos tauru
7	1096	93.4	230	1 CLD2_MOUSE	O68552 mus musculu
8	1096	93.4	230	2 BAB23725	Bab23725 mus muscu
9	571	48.6	239	1 CLD6_HUMAN	O95500 homo sapien
10	571	48.6	239	2 AAR05858	Aar05858 homo sapi
11	571	48.6	239	2 AAR05859	Aar05859 homo sapi
12	571	48.6	239	2 CAD97762	Cad97762 homo sapi
13	571	48.6	239	2 CAD97763	Cad97763 homo sapi
14	561.5	47.8	239	1 CLD6_MOUSE	O92063 mus musculu
15	514	43.8	266	2 O6E5T4	O6E5T4 fugu rubrip
16	507.5	43.2	236	2 O6GME4	O6GME4 xenopus lae
17	461.5	39.3	216	2 O6E5S0	O6E5S0 fugu rubrip
18	460.5	39.2	210	2 O6E5R5	O6E5R5 fugu rubrip
19	459.5	39.1	208	1 CLD4_BRARE	O94991 brachydanic
20	459.5	39.1	213	2 O6DJ92	O6DJ92 xenopus tro
21	456	38.8	218	2 O90XR2	O90XR2 brachydanic
22	456	38.8	218	2 AAH65424	Aah65424 brachydanic
23	455	38.8	219	2 Q765N9	Q765N9 bos tauru
24	455	38.8	219	2 BAD01113	Bad01113 bos tauru
25	453	38.5	211	2 O6E5T5	O6E5T5 fugu rubrip
26	452	38.5	213	2 O7ZS22	O7ZS22 xenopus lae
27	451	38.4	210	2 O6E5G4	O6E5G4 fugu rubrip
28	450.5	38.4	218	1 CLD3_CANFA	Q95K66 canis fami
29	450.5	38.4	223	1 O6E5R9	O6E5R9 fugu rubrip
30	450	38.3	220	1 CLD3_HUMAN	O15551 homo sapien
31	450	38.3	220	2 AAS07555	Aas07555 homo sapi

32	448.5	38.2	219	2 Q81019	Q81019 mus musculu
33	448	38.2	213	2 Q805G0	Q805G0 xenopus lae
34	447.5	38.1	211	2 O6E5R7	O6E5R7 fugu rubrip
35	446	38.0	210	1 CLD4_MOUSE	O35054 mus musculu
36	446	38.0	215	2 O90XR8	O90XR8 brachydanic
37	444.5	37.9	209	2 O90XR9	O90XR9 brachydanic
38	444.5	37.9	209	2 AAH62846	Aah62846 brachydanic
39	443.5	37.8	209	1 CLD4_CERAE	O19005 cercopithec
40	443.5	37.8	214	2 O6PBE4	O6PBE4 xenopus tro
41	443.5	37.8	214	2 AAH59750	Aah59750 xenopus t
42	443	37.7	219	1 CLD6_MOUSE	O92622 mus musculu
43	442.5	37.7	209	1 CLD4_HUMAN	O14493 homo sapien
44	442.5	37.7	209	1 AAP35635	Aap35635 homo sapi
45	442.5	37.7	209	2 AAS07556	Aas07556 homo sapi

## ALIGNMENTS

RESULT 1  
CLD2\_HUMAN  
ID CLD2\_HUMAN STANDARD; PRT; 230 AA.  
AC P57739;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Claudin-2 (UNQ705/PRO1356) (SP82).  
GN Name=CLD2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Epithelium;  
RA Reinecker H.-C., Sakaguchi T., Golden H.M.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell growth."  
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu O., Hase P.B., Heidens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Lao D., Mark W., Robble B., Sanchez C., Scheinfeld J.,  
RA Seehagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."  
RT Genome Res. 13:2265-2270(2003).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Heath P.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,  
RA Kuanerberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,



RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywniński M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
RC TISSUE=Skin and meninges pool- skin;  
RA Strauberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC071747; AAH1747.1;  
SQ SEQUENCE 230 AA; 24548 MW; 52CA642D4A62B70D CRC64;

Query Match 100.0%; Score 1174; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1,3e-90;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120  
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPSDKMFEIGALYIGIISLFLSGLIIT 180  
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPSDKMFEIGALYIGIISLFLSGLIIT 180  
QY 181 LCFSSCSQRNRSNVYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNVYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230

#### RESULT 4

ID CLD2\_CANFA STANDARD; PRT; 230 AA.  
AC Q95KM6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Claudin-2.  
GN Name=CLDN2;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=21206012; PubMed=11309408;  
RA Furness M., Furness K., Saeki H., Tsukita S.,  
RT "Conversion of zonulae occludentes from tight to leaky strand type by  
RT introducing claudin-2 into Madin-Darby canine kidney I cells";  
RL J. Cell Biol. 153:263-272(2001).  
CC -1- FUNCTION: Component of tight junction (TJ) strands.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to the claudin family.

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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC EMBL: AF58907; AAK51433.1;  
DR InterPro: IPR006187; Claudin.  
DR InterPro: IPR005411; Claudin.  
DR InterPro: IPR006188; Claudin\_reg.  
DR InterPro: IPR004031; BMP22\_Claudin.

DR Pfam: PF00822; BMP22\_Claudin.1.  
DR PRINTS: PRO1077; CLAUDIN.  
DR PRINTS: PRO1589; CLAUDIN2.  
DR PROSITE: PS01346; CLAUDIN.1.  
KW Tight junction; Transmembrane.

FT TRANSMEM 8 28 Potential.  
FT TRANSMEM 82 102 Potential.  
FT TRANSMEM 117 137 Potential.  
FT TRANSMEM 163 183 Potential.  
SQ SEQUENCE 230 AA; 24502 MW; 91B71C1B5C0C4BE9 CRC64;

Query Match 95.3%; Score 1119; DB 1; Length 230;  
Best Local Similarity 93.5%; Pred. No. 5.3e-86;  
Matches 215; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120  
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPSDKMFEIGALYIGIISLFLSGLIIT 180  
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDYSPPLVPSDKMFEIGALYIGIISLFLSGLIIT 180  
QY 181 LCFSSCSQRNRSNVYDAYOAOPLATRSSPRGQPPKXSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSDYDYOAOPLATRGSPRPQPPKXSEFNSYSLTGYV 230

#### RESULT 5

ID O76SPL PRELIMINARY; PRT; 230 AA.  
AC O76SPL;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Claudin 2.  
GN Name=CLDN2;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Ohta H., Takiguchi M., Inaba M.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB115779; BAD0111.1;  
DR InterPro: IPR006187; Claudin.  
DR InterPro: IPR005411; Claudin.  
DR InterPro: IPR006188; Claudin\_reg.  
DR InterPro: IPR004031; BMP22\_Claudin.  
DR Pfam: PF00822; BMP22\_Claudin.1.  
DR PRINTS: PRO1077; CLAUDIN.  
DR PRINTS: PRO1589; CLAUDIN2.  
DR PROSITE: PS01346; CLAUDIN.1.  
KW Transmembrane.

SQ SEQUENCE 230 AA; 24533 MW; ED241778B0E541CA CRC64;

Query Match 94.9%; Score 1114; DB 2; Length 230;  
Best Local Similarity 93.9%; Pred. No. 1.4e-85;  
Matches 216; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASIGQLVGYIIGLIGLGLTVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSSAISLACTISVGMCTVFCQDSRAKDRVAVA 120



Db 61 ITCCDIYSTWLG.PADIQAAMWTSASMSLACTIVSVGMCTVFPQESRAKRVAVV 120  
 QY 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 Db 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 QY 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230  
 Db 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230

RESULT 6  
 BAD01111 PRELIMINARY; PRT; 230 AA.  
 ID BAD01111  
 AC BAD01111  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Claudin 2.  
 GN CLDN2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ohta H., Takiguchi M., Inaba M.;  
 RT "Localization of claudin proteins in bovine kidneys.";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 SQ SEQUENCE 230 AA; 2453 MW; ED241778B0541CA CRC64;

Query Match 94.9%; Score 1114; DB 2; Length 230;  
 Best Local Similarity 93.9%; Pred. No. 1,4e-85;  
 Matches 216; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTGLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
 Db 1 MASLGQLVGYIIGLGLGLTGLTGLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
 QY 61 ITCCDIYSTWLG.PADIQAAMWTSASMSLACTIVSVGMCTVFPQESRAKRVAVV 120  
 Db 61 ITCCDIYSTWLG.PADIQAAMWTSASMSLACTIVSVGMCTVFPQESRAKRVAVV 120  
 QY 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 Db 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 QY 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230  
 Db 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230

RESULT 7  
 CLD2\_MOUSE STANDARD; PRT; 230 AA.  
 ID CLD2\_MOUSE  
 AC 088552;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Claudin-2.  
 GN Name=CLDN2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98311639; PubMed=9647647;  
 RA Furness M., Fujita K., Hiltaghi T., Fujimoto K., Tsukita S.;  
 RT "Claudin-1 and -2: novel integral membrane proteins localizing at

RT tight junctions with no sequence similarity to occludin.";  
 RL J. Cell Biol. 141:1539-1550(1998).  
 CC -1- FUNCTION: Component of tight junction (TJ) strands.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the claudin family.

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 CC -----  
 DR EMBL; AF072128; AAC27079.1; -.  
 DR MGD; MGI:1276110; Cldn2.  
 DR InterPro; IPR006187; Claudin.  
 DR InterPro; IPR005411; Claudin2.  
 DR InterPro; IPR006188; Claudin2\_reg.  
 DR Pfam; PF00822; PMP22\_Claudin; 1.  
 DR PRINTS; PR01077; CLAUDIN.  
 DR PRINTS; PR01598; CLAUDIN2.  
 DR PROSITE; PS01346; CLAUDIN; 1.  
 DR Tight junction; Transmembrane.  
 KW TRANSMEM 8 28  
 FT TRANSMEM 82 102 Potential.  
 FT TRANSMEM 117 137 Potential.  
 FT TRANSMEM 163 183 Potential.  
 SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match 93.4%; Score 1096; DB 1; Length 230;  
 Best Local Similarity 91.3%; Pred. No. 4.5e-94;  
 Matches 210; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTGLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
 Db 1 MASLGQLVGYIIGLGLGLTGLTGLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
 QY 61 ITCCDIYSTWLG.PADIQAAMWTSASMSLACTIVSVGMCTVFPQESRAKRVAVV 120  
 Db 61 ITCCDIYSTWLG.PADIQAAMWTSASMSLACTIVSVGMCTVFPQESRAKRVAVV 120  
 QY 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 Db 121 GGVFLLIGLGLGPIPAVMNLHGILRDPYSPVPSDKMFEIGALYGIISLSLGIAT 180  
 QY 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230  
 Db 181 LCFSCSGQRNRSNYDAYQAOPLATRSSPPRGQPKKSEFNSYSILGYV 230

RESULT 8  
 BAB23725 PRELIMINARY; PRT; 230 AA.  
 ID BAB23725  
 AC BAB23725;  
 DT 14-APR-2004 (T-EMBLrel. 27, Created)  
 DT 14-APR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Adult male liver cDNA, RIKEN full-length enriched library,  
 DE clone:1300013G06 product:claudin 2, full insert sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";

Query Match            93.4%; Score 1096; DB 2; Length 230;  
Best Local Similarity 91.3%; Pred. No. 4,5e-84;  
Matches 210; Conservative 11; Mismatches 9; Indels 0; Gaps 0

RN Nature 420:563-573 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=21085660; PubMed=11217851;  
RT RIKEN FANTOM Consortium;  
RL "Functional annotation of a full-length mouse cDNA collection."  
RN Nature 409:665-690(2001).  
[3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Mech. Enzymol. 303:19-44(1999).  
[4]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
Ra Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076661;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Ra Kono H., Akiyama Y., Nishi K., Kitsumai T., Tashtiro H., Itoh M.,  
Ra Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwara S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe K.,  
Ra Umeda Y., Ishikawa T., Togawa K., Tanaka T., Matsura S., Kawai J.,  
Ra Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multichannel sequencer."  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA Adachi T., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,  
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
Ra Hanagaki T., Hara A., Hayatsu N., Hitomoto K., Hirooka T., Horii F.,  
Ra Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
Ra Kawai J., Koima Y., Kono H., Kouda M., Koyasu S., Kurihara C.,  
Ra Matsuyama T., Miyazaki A., Nihei K., Nomura K., Nunazaki R., Ono M.,  
Ra Okazaki Y., Okido T., Owa C., Satou K., Satoh R., Sakai C., Sakai K.,  
Saio H., Sasaki D., Shibata K., Shibata K., Shinagawa A., Shiraki T.,  
Ra Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
Ra Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
Ra Muramatsu M., Hayashizaki Y.;  
RL Submitted (Jul-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL, AK004990; BAB33725.1; 38A7C074A1B0D5D2 CRC64;  
SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1B0D5D2 CRC64;

1 MASLGLQVGVYIGLLGILGLTVAMLLPSKTSSTSYGASITVAAGPFSKLMMECATHSYG 60  
Db 1 MASLGLQVGVYIGLLGILGLTISIAMLLPMKRSSSYGASITVAAGPFSKLMMECATHSYG 60  
Qy ITCCGYSTLGLLPDIQAQAQMNTSSATSLACISIVNGRCYVFCQESPAKDRAVAA 120  
Db 61 ITCCGYSTLGLLPDIQAQAQMNTSSATSLACISIVNGRCYVFCQDSAPKORAVAY 120  
Qy ITCCGYSTLGLLPDIQAQAQMNTSSATSLACISIVNGRCYVFCQESPAKDRAVAA 120  
Db 121 GGVPFIIIGLGIIFVANWMLHGILTRDFSPPLVPDSKKPEIGEGALTYLGIISSLFSLIAGII 180  
Qy 121 GGVPFIIIGLGIIFVANWMLHGILTRDFSPPLVPDSKKPEIGEGALTYLGIISSLFSLIAGII 180  
Db 121 GGVPFIIIGLGIIFVANWMLHGILTRDFSPPLVPDSKKPEIGEGALTYLGIISSLFSLIAGII 180  
Qy 161 LCFSCSGSQRNRNSNYDAVOAQFLATRBSRPQPQPPKVMSSEFNYSYLITGVY 230

181 LCPSCSPQGNRTNYYDGYQAOPIATSSSPSAQOPAKSEFNSYSLGYV 230

RESULT 9

ID	CLIDE	HUMAN	STANDARD;	PRT;	239 AA.
DC	095500;				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	05-JUN-2004 (Rel. 44, Last annotation update)				
DE	Claudin-14 (UNQ771/PRO1571).				
GN	Name=CLDN14;				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
CC	NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A.				
RA	Keen T.J., Inglehearn C.F.;				
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBD databases.				
RP	SEQUENCE FROM N.A., AND VARIANT DFNB29 ASP-85.				
RP	TISSUE=Liver;				
RC	MEDLINE=21097730; PubMed=1163249;				
RC	Milcox E.R., Burton Q.L., Nar S., Riazuddin S., Smith T.N.,				
RA	Pioplis B., Belyantseva J., Ben-Yosef T., Liburd N.A., Morell R.J.,				
RA	Kachar B., Wu D.K., Griffith A.J., Riazuddin S., Friedman T.B.;				
RT	"Mutations in the gene encoding tight junction claudin-14 cause				
RT	autosomal recessive deafness DFNB29."				
RL	Cell 104:165-172 (2001).				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;				
RC	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Dowd P.,				
RA	Batton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Levis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,				
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,				
RA	Vanclan R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P., Gray A.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment."				
RL	Genome Res. 13:2265-2270(2003).				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=20289799; PubMed=10830953;				
RC	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,				
RA	Park H.-S., Toyoda A., Ishii K., Tokuoki Y., Choi D.-K., Groner Y.,				
RA	Soda E., Ohki M., Takagi T., Sakaki Y., Tauden S., Blechschmidt K.,				
RA	Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,				
RA	Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,				
RA	Reichenthal A., Kudon J., Shibuya K., Kawasaki K., Asakawa S.,				
RA	Shintani A., Saeki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,				
RA	Shimoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,				
RA	Ramette M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,				
RA	Santer J., Beck A., Klages S., Hennig S., Riesselmann L., Dagsen E.,				
RA	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,				
RA	Lehrach H., Reinhardt R., Jaepo M.-U.;				
RT	"The DNA sequence of human chromosome 21."				
RL	Nature 405:311-319(2000).				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Skin;				
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RC	Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Stausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Caminci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly C.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunarene P.H.,  
 RA Rha S.S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences." J.  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6].  
 RP VARIANT MET-4.  
 RX MEDLINE=22675606; PubMed=12791041;  
 RA Uyguner O., Emiroglu M., Uzuncu A., Hafiz G., Ghanbari A., Baerger N.,  
 RA Yiksel-Apak M., Wollnik B.;  
 RT "Frequencies of gap- and tight-junction mutations in Turkish families  
 RT with autosomal-recessive non-syndromic hearing loss." J.  
 RL Clin. Genet. 64:65-69(2003).  
 CC -1- FUNCTION: Component of tight junction (TJ) strands.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Liver, kidney. Also found in ear.  
 CC -1- DISEASE: Defects in CLDN14 are the cause of an autosomal recessive  
 CC form of nonsyndromic sensorineural deafness (DFNB29) [MIM:605608].  
 CC -1- SIMILARITY: Belongs to the claudin family.  
 CC -----  
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 CC -----  
 DR EMBL/ AJ132445; CAA10669.1; -;  
 DR EMBL/ AF314090; AAG60052.1; -;  
 DR EMBL/ AY358533; AAG88987.1; -;  
 DR EMBL/ AP001726; BA955509.1; -;  
 DR EMBL/ BC012126; AAH12126.1; -;  
 DR Genew; HGNC:2035; CLDN14.  
 DR MIM; 605608; -;  
 DR GO; GO:0006461; P:Protein complex assembly; TAS.  
 DR Interpro; IPR006187; Claudin.  
 DR Interpro; IPR006188; Claudin\_reg.  
 DR Interpro; IPR004031; PMP22\_Claudin.  
 DR Pfam; PF00822; PMP22\_Claudin; 1.  
 DR PRINTS; PR01077; CLAUDIN.  
 DR PROSITE; PS01346; CLAUDIN; 1.  
 KM Deafness; Disease mutation; Polymorphism; Tight junction;  
 KM Transmembrane.  
 FT TRANSMEM 8 28 Potential.  
 FT TRANSMEM 82 102 Potential.  
 FT TRANSMEM 116 136 Potential.  
 FT TRANSMEM 163 183 Potential.  
 FT VARIANT 4 4 T->M.  
 FT VARIANT 85 85 /FTID=VAR\_017227.  
 FT VARIANT V->D (in DFNB29).  
 FT VARIANT /FTID=VAR\_010738.  
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;  
 Query Match 48.6%; Score 571; DB 1; Length 239;  
 Best Local Similarity 46.8%; Pred. No. 6e-40; Indels 12; Gaps 3;  
 Matches 11; Conservative 44; Mismatches 70;  
 QY 1 MASTGLQVYIGLGLGTLVAMLLPMSKTSYVGSIVTAVGFSKGLMECATSTG 60  
 DB 1 MASTAVQLGLFLSFLGVMGTLITLLPHMRRTAVGNTILFVSYLKGLMECVHSTG 60  
 QY 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMCRCTFCQESRAKRVVA 120  
 DB 1 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMCRCTFCQESRAKRVVA 120  
 QY 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 DB 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 QY 61 IYCCQIYRSLALPDLQARALMVISCLSGIACAVIAGKCTRCAGTPAKTTFALL 120  
 DB 61 IYCCQIYRSLALPDLQARALMVISCLSGIACAVIAGKCTRCAGTPAKTTFALL 120  
 QY 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 DB 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 QY 181 LCFSCSSQRRNSRYDAYQAOLATRSSPPG---QPRVKSSEFNSYSLT----GY 229  
 DB 181 LCFSCSSQRRNSRYDAYQAOLATRSSPPG---QPRVKSSEFNSYSLT----GY 229  
 QY 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGY 233  
 DB 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGY 233  
 RESULT 10  
 AAR05858 PRELIMINARY; PRT; 239 AA.  
 ID AAR05858; PRELIMINARY; PRT; 239 AA.  
 AC AAR05858; PRELIMINARY; PRT; 239 AA.  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Claudin 14 beta isoform.  
 GN CLDN14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Battenhofer M., Falciola V., Charollais A., Caille D., Borel C.,  
 RA Battivili X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.,  
 RT "Claudin 14 and deafness." J.  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBS databases.  
 DR EMBL/ AY355348; AAR05858.1; -;  
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7FD0E09A CRC64;  
 Query Match 48.6%; Score 571; DB 2; Length 239;  
 Best Local Similarity 46.8%; Pred. No. 6e-40;  
 Matches 11; Conservative 44; Mismatches 70; Indels 12; Gaps 3;  
 QY 1 MASTGLQVYIGLGLGTLVAMLLPMSKTSYVGSIVTAVGFSKGLMECATSTG 60  
 DB 1 MASTAVQLGLFLSFLGVMGTLITLLPHMRRTAVGNTILFVSYLKGLMECVHSTG 60  
 QY 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMCRCTFCQESRAKRVVA 120  
 DB 61 ITQCDIYSTLLGLPADIQAAMVNTSSAISLACIISVGMCRCTFCQESRAKRVVA 120  
 QY 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 DB 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 QY 61 IYCCQIYRSLALPDLQARALMVISCLSGIACAVIAGKCTRCAGTPAKTTFALL 120  
 DB 61 IYCCQIYRSLALPDLQARALMVISCLSGIACAVIAGKCTRCAGTPAKTTFALL 120  
 QY 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 DB 121 GGVFFILGGLGFIPIAMNHLGIRDFYSPVLVDSKFEIGALYGLISLFSLIAGIT 180  
 QY 181 LCFSCSSQRRNSRYDAYQAOLATRSSPPG---QPRVKSSEFNSYSLT----GY 229  
 DB 181 LCFSCSSQRRNSRYDAYQAOLATRSSPPG---QPRVKSSEFNSYSLT----GY 229  
 QY 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGY 233  
 DB 181 LCLSCQDEAP---YRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGY 233  
 RESULT 11  
 AAR05859 PRELIMINARY; PRT; 239 AA.  
 ID AAR05859; PRELIMINARY; PRT; 239 AA.  
 AC AAR05859; PRELIMINARY; PRT; 239 AA.  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Claudin 14 epsilon isoform.  
 GN CLDN14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Battenhofer M., Falciola V., Charollais A., Caille D., Borel C.,  
 RA Battivili X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.,  
 RT "Claudin 14 and deafness." J.

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY55349; AAR0589.1; -  
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7D0E09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;  
 Best Local Similarity 46.8%; Pred. No. 6e-40;  
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGLQVGYIIGLGLGLTIVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASTAVQLGFLSPFLGAVGTLLITLPHMRRTAHVGNILITAVSYLKGIMCECWHSTG 60  
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQSRADRYAVA 120  
 DB 61 IYCCQIRSLALPQDIOAARALMVISLISGLACAVIGMCKTRCAKGTPTTFAIL 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKFEIGALYIGIISLFLINGII 180  
 DB 121 GGTLPILAGLCLMVAWSMTTNDVQNFYNPFLPSGKFEIGQALYIGFISLSLIGTL 180  
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYLT-----GY 229  
 DB 181 LCISQCDQAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

## RESULT 12

CAD97762 PRELIMINARY; PRT; 239 AA.

ID CAD97762; PRELIMINARY; PRT; 239 AA.  
 AC CAD97762; (TREMUREL. 27, Created)  
 DT 02-MAR-2004 (TREMUREL. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMUREL. 27, Last sequence update)  
 DE Claudin 14.  
 GN CLDN14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Placenta;  
 RA Wattenhofer M., Falcioia V., Charollais A., Calle D., Borel C.,  
 RA Berville X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.;  
 RT "Claudin 14 and deafness";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ56765; CAD97762.1; -  
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7D0E09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;  
 Best Local Similarity 46.8%; Pred. No. 6e-40;  
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGLQVGYIIGLGLGLTIVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASTAVQLGFLSPFLGAVGTLLITLPHMRRTAHVGNILITAVSYLKGIMCECWHSTG 60  
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQSRADRYAVA 120  
 DB 61 IYCCQIRSLALPQDIOAARALMVISLISGLACAVIGMCKTRCAKGTPTTFAIL 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKFEIGALYIGIISLFLINGII 180  
 DB 121 GGTLPILAGLCLMVAWSMTTNDVQNFYNPFLPSGKFEIGQALYIGFISLSLIGTL 180  
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYLT-----GY 229  
 DB 181 LCISQCDQAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 13  
 CAD97763 PRELIMINARY; PRT; 239 AA.  
 ID CAD97763; PRELIMINARY; PRT; 239 AA.  
 AC CAD97763;

DT 02-MAR-2004 (TREMUREL. 27, Created)  
 DT 02-MAR-2004 (TREMUREL. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMUREL. 27, Last sequence update)  
 DE Claudin 14.

GN CLDN14.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Testis;  
 RA Wattenhofer M., Falcioia V., Charollais A., Calle D., Borel C.,  
 RA Berville X., Petersen M.B., Antonarakis S.E., Meda P., Raymond A.;  
 RT "Claudin 14 and deafness";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ56766; CAD97763.1; -  
 SQ SEQUENCE 239 AA; 25699 MW; DD41652F7D0E09A CRC64;

Query Match 48.6%; Score 571; DB 2; Length 239;  
 Best Local Similarity 46.8%; Pred. No. 6e-40;  
 Matches 111; Conservative 44; Mismatches 70; Indels 12; Gaps 3;

QY 1 MASIGLQVGYIIGLGLGLTIVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASTAVQLGFLSPFLGAVGTLLITLPHMRRTAHVGNILITAVSYLKGIMCECWHSTG 60  
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQSRADRYAVA 120  
 DB 61 IYCCQIRSLALPQDIOAARALMVISLISGLACAVIGMCKTRCAKGTPTTFAIL 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKFEIGALYIGIISLFLINGII 180  
 DB 121 GGTLPILAGLCLMVAWSMTTNDVQNFYNPFLPSGKFEIGQALYIGFISLSLIGTL 180  
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYLT-----GY 229  
 DB 181 LCISQCDQAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

## RESULT 14

CLDN\_MOUSE STANDARD; PRT; 239 AA.

ID CLDN\_MOUSE; STANDARD; PRT; 239 AA.  
 AC 092053; 09D284;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Claudin-14.  
 GN Name=CLDN14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Liver;  
 RA Morita K., Furuse M., Tsukita S.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

QY 1 MASIGLQVGYIIGLGLGLTIVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASTAVQLGFLSPFLGAVGTLLITLPHMRRTAHVGNILITAVSYLKGIMCECWHSTG 60  
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQSRADRYAVA 120  
 DB 61 IYCCQIRSLALPQDIOAARALMVISLISGLACAVIGMCKTRCAKGTPTTFAIL 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKFEIGALYIGIISLFLINGII 180  
 DB 121 GGTLPILAGLCLMVAWSMTTNDVQNFYNPFLPSGKFEIGQALYIGFISLSLIGTL 180  
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYLT-----GY 229  
 DB 181 LCISQCDQAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

QY 1 MASIGLQVGYIIGLGLGLTIVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASTAVQLGFLSPFLGAVGTLLITLPHMRRTAHVGNILITAVSYLKGIMCECWHSTG 60  
 QY 61 ITCCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQSRADRYAVA 120  
 DB 61 IYCCQIRSLALPQDIOAARALMVISLISGLACAVIGMCKTRCAKGTPTTFAIL 120  
 QY 121 GGVFFILGGLGFIPIVAMNHLGILRDPYSPVPSDKFEIGALYIGIISLFLINGII 180  
 DB 121 GGTLPILAGLCLMVAWSMTTNDVQNFYNPFLPSGKFEIGQALYIGFISLSLIGTL 180  
 QY 181 LCFSCSSQRRNSNYDAYOAPLATRSSPRG---QPPKVSFNYSYLT-----GY 229  
 DB 181 LCISQCDQAP---YRPYQAPPRATTTTANTAPAYQPPAAYKONRAPSVTSATHSY 233

RESULT 15  
 CAD97763 PRELIMINARY; PRT; 239 AA.  
 ID CAD97763; PRELIMINARY; PRT; 239 AA.  
 AC CAD97763;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Colon; DOI=10.1038/nature01266;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kanakawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakado I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,  
 RA Schirml L.M., Kanapin A., Macsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brucic V., Choithia C., Corbani L.E., Cousins S.,  
 RA Dalia E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Guenlinich S., Hirokawa N., Jackson I.J., Jaryls E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Meglot D.R., Meltz L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petre G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Varardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilmink L.G., Wyrshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Zimnicki P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Haseizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Venauteh A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs.  
 CC -1- FUNCTION: Component of tight junction (TJ) strands.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: At postnatal day 4, expression is apically  
 CC located in the inner and outer hair cell region of the entire  
 CC organ of corti. By postnatal day 8, expression is highest in the  
 CC sensory cells of the organ of corti and present in all other  
 CC sensory epithelia of the inner ear vestibular organs. Also  
 CC expressed in liver and kidney.  
 CC -1- SIMILARITY: Belongs to the claudin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AF124429; AADI7323.1; -;  
 DR EMBL: AF114089; AAG60051.2; -;  
 DR EMBL: AK020255; BAB32041.1; -;  
 DR MGD: MGI:1860425; C1dn14.  
 DR InterPro: IPR006187; Claudin.  
 DR InterPro: IPR006188; Claudin reg.  
 DR Pfam: PF00832; PMP22 Claudin.  
 DR PRINTS: PRO1077; CLAUDIN.  
 DR PROSITE: PS01346; CLAUDIN; 1.  
 KW Tight junction; Transmembrane.  
 DR TRANSMEM 8 28 Potential.  
 FT TRANSMEM 82 102 Potential.  
 FT TRANSMEM 116 136 Potential.  
 FT TRANSMEM 163 183 Potential.  
 FT TRANSMEM 115 115 T -> N (in Ref. 1).  
 FT TRANSMEM 119 119 V -> M (in Ref. 4).  
 FT TRANSMEM 129 129 G -> A (in Ref. 1).  
 FT TRANSMEM 166 166 L -> M (in Ref. 1).  
 FT TRANSMEM 187 187 D -> E (in Ref. 1).  
 SQ SEQUENCE 239 AA; 25614 MW; 24DE6A6DA56B61 CRC64;

Query Match 47.8%; Score 561.5; DB 1; Length 239;  
 Best Local Similarity 46.9%; Pred. No. 3.8e-39;  
 Matches 112; Conservative 43; Mismatches 75; Indels 9; Gaps 3;  
 QY 1 MASLGLVYILGLGLGLTVAAMLPSMKTSYVYASIVYAVGSKGIMMECATHSIG 60  
 DB 1 MASLGLVYILGLGLGLTVAAMLPSMKTSYVYASIVYAVGSKGIMMECATHSIG 60  
 QY 61 ITQCDDYSTLLGLPADIOAQAAMVTSSAIISSLAIIISVYKCTVFCOSRAKORVAVA 120  
 DB 61 ITQCDDYSTLLGLPADIOAQAAMVTSSAIISSLAIIISVYKCTVFCOSRAKORVAVA 120  
 QY 121 GGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 180  
 DB 121 GGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 180  
 QY 181 LCFSSCSQRNRSYVAYQAQPLATSSP--RP-----GQPKVSEFNS-YSLNGVY 230  
 DB 181 LCFSSCSQRNRSYVAYQAQPLATSSP--RP-----GQPKVSEFNS-YSLNGVY 230  
 DB 181 LCLSCDEAPRYPPQSRAGATTATAPAYRPPAAYKONRAPSVAHSGIRLNDVY 239

## RESULT 15

Q6EST4 PRELIMINARY; PRT; 266 AA.  
 AC Q6EST4; 28, Created (28, 01-OCT-2004 (TREMBLrel. 28, Last sequence update))  
 DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DE Claudin 2.  
 OS Name-clnd2;  
 GN Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15197168;  
 RA Loh Y.H., Christoffele A., Brenner S., Hunziker W., Venkatesh B.;  
 RT "Extensive Expansion of the Claudin Gene Family in the Teleost Fish,  
 Fugu rubripes".  
 RL Genome Res. 14:1248-1257(2004).  
 DR EMBL: AY554353; AAT64079.1; -;  
 SQ SEQUENCE 266 AA; 28016 MW; 23BE3D7DOA0F89A4 CRC64;

Query Match 43.8%; Score 514; DB 2; Length 266;  
 Best Local Similarity 49.3%; Pred. No. 4.1e-35;  
 Matches 99; Conservative 41; Mismatches 53; Indels 8; Gaps 3;

QY 1 MASLGLVYILGLGLGLTVAAMLPSMKTSYVYASIVYAVGSKGIMMECATHSIG 60  
 DB 1 MASLGLVYILGLGLGLTVAAMLPSMKTSYVYASIVYAVGSKGIMMECATHSIG 60  
 QY 61 ITQCDDYSTLLGLPADIOAQAAMVTSSAIISSLAIIISVYKCTVFCOE--SRADRYA 118  
 DB 61 ITQCDDYSTLLGLPADIOAQAAMVTSSAIISSLAIIISVYKCTVFCOE--SRADRYA 118  
 QY 61 AFQCFYNSMLAPSPMOASRALMVISLIVSLIAIMAVIGMQCTV-CIEGLAVAGRYA 119  
 DB 61 AFQCFYNSMLAPSPMOASRALMVISLIVSLIAIMAVIGMQCTV-CIEGLAVAGRYA 119  
 QY 119 VAGGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 178  
 DB 119 VAGGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 178  
 QY 120 GGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 179  
 DB 120 GGVFFILGLGLFIPVAMNLHGLRDPYSPPLVDSKKEFGALVYIGTISLFLIAGTI 179  
 QY 179 IILFSCSSQ-----RNRSNY 194  
 DB 180 GMLCVSCSEENDGRNRNGRY 200

Search completed: October 27, 2004, 07:21:04  
 Job time: 198 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:36:34 ; Search time 128 Seconds  
(without alignments)  
582.575 Million cell updates/sec

Title: US-09-787-677A-3

Sequence: 1 MASLGLVGYILGLGLG.....PCGPKVKSBNFSYLTGYV 230

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1370721 seqs, 324215800 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
7: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
8: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	230	9	US-09-998-598-2590
2	230	100.0	230	10	US-09-888-257A-6
3	230	100.0	230	10	US-09-946-374-134
4	230	100.0	230	11	US-09-833-245-1256
5	230	100.0	230	11	US-09-978-360A-698
6	230	100.0	230	13	US-10-063-551-80
7	230	100.0	230	13	US-10-063-551-80
8	230	100.0	230	13	US-10-063-551-80
9	230	100.0	230	14	US-10-028-072-492
10	230	100.0	230	14	US-10-063-616-80
11	230	100.0	230	14	US-10-140-808-492
12	230	100.0	230	14	US-10-063-569-80
13	230	100.0	230	14	US-10-063-513-80

14	230	100.0	230	14	US-10-063-515-80	Sequence 80, Appl
15	230	100.0	230	14	US-10-063-512-80	Sequence 80, Appl
16	230	100.0	230	14	US-10-121-049-492	Sequence 492, Appl
17	230	100.0	230	14	US-10-123-904-492	Sequence 492, Appl
18	230	100.0	230	14	US-10-140-470-492	Sequence 492, Appl
19	230	100.0	230	14	US-10-063-502-80	Sequence 80, Appl
20	230	100.0	230	14	US-10-175-746-492	Sequence 492, Appl
21	230	100.0	230	14	US-10-176-918-492	Sequence 492, Appl
22	230	100.0	230	14	US-10-176-921-492	Sequence 492, Appl
23	230	100.0	230	14	US-10-063-549-80	Sequence 80, Appl
24	230	100.0	230	14	US-10-137-865-492	Sequence 492, Appl
25	230	100.0	230	14	US-10-140-474-492	Sequence 492, Appl
26	230	100.0	230	14	US-10-142-419-492	Sequence 492, Appl
27	230	100.0	230	14	US-10-143-114-492	Sequence 492, Appl
28	230	100.0	230	14	US-10-140-002-492	Sequence 492, Appl
29	230	100.0	230	14	US-10-063-554-80	Sequence 80, Appl
30	230	100.0	230	14	US-10-006-856A-134	Sequence 134, Appl
31	230	100.0	230	14	US-10-142-419-492	Sequence 492, Appl
32	230	100.0	230	14	US-10-063-553-80	Sequence 80, Appl
33	230	100.0	230	14	US-10-063-518-80	Sequence 80, Appl
34	230	100.0	230	14	US-10-123-262-492	Sequence 492, Appl
35	230	100.0	230	14	US-10-142-423-492	Sequence 492, Appl
36	230	100.0	230	14	US-10-063-598-80	Sequence 80, Appl
37	230	100.0	230	14	US-10-227-693-80	Sequence 80, Appl
38	230	100.0	230	14	US-10-006-818A-134	Sequence 134, Appl
39	230	100.0	230	14	US-10-121-050-492	Sequence 492, Appl
40	230	100.0	230	14	US-10-141-755-492	Sequence 492, Appl
41	230	100.0	230	14	US-10-143-037-492	Sequence 492, Appl
42	230	100.0	230	14	US-10-063-563-80	Sequence 80, Appl
43	230	100.0	230	14	US-10-006-485A-134	Sequence 134, Appl
44	230	100.0	230	14	US-10-013-907A-134	Sequence 134, Appl
45	230	100.0	230	14	US-10-015-499A-134	Sequence 134, Appl

## ALIGNMENTS

RESULT 1  
US-09-998-598-2590  
Sequence 2590, Application US/09998598  
Patent No. US20020150922A1  
GENERAL INFORMATION:  
APPLICANT: Stoik, John A.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Chenault, Ruth A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.561  
CURRENT APPLICATION NUMBER: US/09/998,598  
CURRENT FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 2606  
SOFTWARE: Corixa Invention Disclosure Database  
SEQ ID NO 2590  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-998-598-2590

Query Match 100.0%; Score 230; DB 9; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASLGLVGYILGLGLGLVAMLLPSWKTSYVGASIVRAVGRSGKGLMECAHSTG 60  
DB 1 MASLGLVGYILGLGLGLVAMLLPSWKTSYVGASIVRAVGRSGKGLMECAHSTG 60  
QY ITTCDDYSTLGLPADIOAQAAMVTSSAISLACTIISVGRCTVFCQESRAKDRVAVA 120  
DB 61 ITTCDDYSTLGLPADIOAQAAMVTSSAISLACTIISVGRCTVFCQESRAKDRVAVA 120  
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Db 121 GGVFLLGLGLGTFIPVAMNHGLRDFYSLVDSMKFEIGALYLGITISLFSLLAGII 180  
QY 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPKVSEFNSYSLTGYV 230  
Db 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPKVSEFNSYSLTGYV 230

## RESULT 2

US-09-888-257A-6  
; Sequence 6, Application US/09888257A  
; Publication No. US20030060612A1  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Polakis, Paul  
; APPLICANT: Smith, Victoria  
; APPLICANT: Wood, William I.  
; APPLICANT: Wu, Thomas D.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5002R1  
; CURRENT APPLICATION NUMBER: US/09/888,257A  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/063,540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: US 60/089,653  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 60/099,792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/103,678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: US 60/235,451  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: PCT/US99/20111  
; PRIOR FILING DATE: 1999-09-01  
; PRIOR APPLICATION NUMBER: PCT/US00/04342  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: PCT/US01/06666  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 6  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-888-257A-6

Query Match 100.0%; Score 230; DB 10; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MASLGLQVGIYIIGLLGLGLTLVAMLPSTKTSYVGAISVTAVGFSKGLMBCATHTSG 60  
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Db 61 ITCCDIYSTLLGLPADIOAAQAMVNTSSATISLACITISVGMCTVACQESRAKDRVAVA 120

QY 121 GGVFLLGLGLGTFIPVAMNHGLRDFYSLVDSMKFEIGALYLGITISLFSLLAGII 180  
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Db 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPRPGQPKVSEFNSYSLTGYV 230

## RESULT 3

US-09-946-374-134  
; Sequence 134, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tomas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
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; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808



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 PRIOR FILING DATE: 1998-09-24  
 PRIOR APPLICATION NUMBER: 60/101916  
 PRIOR FILING DATE: 1998-09-29  
 PRIOR APPLICATION NUMBER: 60/102207

PRIOR APPLICATION NUMBER: 60/102240  
 PRIOR FILING DATE: 1998-09-29  
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 PRIOR FILING DATE: 1998-10-08  
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 PRIOR FILING DATE: 1998-10-14  
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 PRIOR APPLICATION NUMBER: 60/105002  
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 PRIOR APPLICATION NUMBER: 60/105104  
 PRIOR FILING DATE: 1998-10-21  
 PRIOR APPLICATION NUMBER: 60/105169  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105266  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105693  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105694  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 230; DB 10; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYITGLIGLGLTVAAMLPSWKTSYVYGASIVTAVGSKGLMBCATHSTG 60  
 DB 1 MASLGLQVGYITGLIGLGLTVAAMLPSWKTSYVYGASIVTAVGSKGLMBCATHSTG 60

QY 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
Db 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFLIGLIGLIPVAMNHLGILRDFYSPVDSMKFEIGALYLGIIISLFLIAGII 180  
Db 121 GGVFFLIGLIGLIPVAMNHLGILRDFYSPVDSMKFEIGALYLGIIISLFLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRGQPPKVSSEFNSYSILGYV 230  
Db 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRGQPPKVSSEFNSYSILGYV 230

## RESULT 4

US-09-833-245-1256  
Sequence 1256, Application US/09833245  
Publication No. US20040010134A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PFS46PCT  
CURRENT APPLICATION NUMBER: US/09/833,245  
PRIOR FILING DATE: 2001-04-12, 358  
PRIOR APPLICATION NUMBER: 60/229, 358  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: 60/256, 931  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/199, 384  
PRIOR FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 2267  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1256  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-833-245-1256

Query Match 100.0%; Score 230; DB 11; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGIQVGYIIGLIGLIGLIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
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QY 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
Db 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
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Db 121 GGVFFLIGLIGLIPVAMNHLGILRDFYSPVDSMKFEIGALYLGIIISLFLIAGII 180  
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## RESULT 5

US-09-978-360A-698  
Sequence 698, Application US/09978360A  
Publication No. US20040110939A1  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Jobert, Severin  
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
FILE REFERENCE: 56 USA CIP  
CURRENT APPLICATION NUMBER: US/09/978,360A  
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: US 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: US 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: US 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: US 60/099,273  
PRIOR FILING DATE: -09-04  
PRIOR APPLICATION NUMBER: US 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: US 09/215,435  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: PCT/IB98/02122  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: US 09/247,155  
PRIOR FILING DATE: 1999-02-09  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 810  
SOFTWARE: Patent.pm  
SEQ ID NO 698  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24..-1  
US-09-978-360A-698

Query Match 100.0%; Score 230; DB 11; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGIQVGYIIGLIGLIGLIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
Db 1 MASLGIQVGYIIGLIGLIGLIVAMLLPSWKTSSYVGASIVTAVGFSKGLMMECATHTSG 60  
QY 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
Db 61 ITQCDISTLLGIPADIOAAMWTSASISLACIISVGMCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFLIGLIGLIPVAMNHLGILRDFYSPVDSMKFEIGALYLGIIISLFLIAGII 180  
Db 121 GGVFFLIGLIGLIPVAMNHLGILRDFYSPVDSMKFEIGALYLGIIISLFLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRGQPPKVSSEFNSYSILGYV 230  
Db 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRGQPPKVSSEFNSYSILGYV 230

## RESULT 6

US-10-006-867-80  
Sequence 80, Application US/10006867  
Publication No. US20020119130A1  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvarcoff, Ellen  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Matanabe, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006,867  
CURRENT FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435

PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106030  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106856  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108807  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/112419  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112853  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113011  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/112854  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113300  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113408  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/114223  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 60/115614  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/116527  
PRIOR FILING DATE: 1999-01-20  
PRIOR APPLICATION NUMBER: 60/116843  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/119285

```

; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR APPLICATION NUMBER: 09/380142

```

```

Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
QY 1 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFTLGLGLGFIPIVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFTLGLGLGFIPIVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSCSSQRNRSNYYDAYQAOPLATRSSPRPGQPKVSEFNSYSLTGYV 230
DB 181 LCFSCSSQRNRSNYYDAYQAOPLATRSSPRPGQPKVSEFNSYSLTGYV 230

```

#### RESULT 7

```

US-10-063-547-80
; Sequence 80, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-547-80

```

```

Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFTLGLGLGFIPIVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
DB 121 GGVFTLGLGLGFIPIVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180
QY 181 LCFSCSSQRNRSNYYDAYQAOPLATRSSPRPGQPKVSEFNSYSLTGYV 230
DB 181 LCFSCSSQRNRSNYYDAYQAOPLATRSSPRPGQPKVSEFNSYSLTGYV 230

```

#### RESULT 8

```

US-10-063-551-80
; Sequence 80, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-551-80

```

```

Query Match 100.0%; Score 230; DB 13; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYITLGLGLGLTIVAMLLPSWKTSYVGAIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
DB 61 ITQCDIYSTLLGLPADIQAAMMTSSAISLACTISVGMKCTVFCQESRAKORVAVA 120
QY 121 GGVFTLGLGLGFIPIVAMNLHGILRDFYSPVLPDSMKFEIGALYIGIISLPSLIAGII 180

```

Db 121 GGVFFILGILGFLPVMNLHGLRDFYSPVLPDSMFEIGEMALYGLIISLFSLLIAGII 180  
Qy 181 LCPSRSSRRSNRYDAYOAPLATRSSPRGCPKXKSEPNYSYLTGYV 230  
Db 181 LCPSRSSRRSNRYDAYOAPLATRSSPRGCPKXKSEPNYSYLTGYV 230

## RESULT 9

US-10-028-072-492  
Sequence 492, Application US/10028072  
Publication No. US2003004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028, 072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081695  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081818  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082999  
PRIOR FILING DATE: 1998-04-24



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C182  
CURRENT APPLICATION NUMBER: US/10/140,808  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 492  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-808-492

Query Match 100.0%; Score 230; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
DB 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
QY 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230

RESULT 12  
US-10-063-569-80  
Sequence 80, Application US/10063569  
Publication No. US20030018168A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,569  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-569-80

Query Match 100.0%; Score 230; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;

Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
DB 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
QY 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230

RESULT 13  
US-10-063-513-80  
Sequence 80, Application US/10063513  
Publication No. US20030018172A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,513  
CURRENT FILING DATE: 2002-05-01  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 80  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-513-80

Query Match 100.0%; Score 230; DB 14; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.8e-207;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
DB 1 MASLGQLVGYITIGLGLGTLVAMLLPSWKTSSYVGASIVTVAVGFSKGLMMECATHTSTG 60  
QY 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGFPADIOAAQAMWVTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
DB 121 GGVFFILGLGFIPIVAMNHLGILRDPYSPVDSMKFEIGALYIGIISLPSLIAGII 180  
QY 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSSQRRNSNYDAYOQAPLATRSSPPGQPPVKSEFNSYSLTGYV 230

RESULT 14  
US-10-063-515-80  
Sequence 80, Application US/10063515  
Publication No. US20030018173A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.



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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-80

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Query Match 100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASLGLQLVGYILGLIGLGLTLVAMLLPSWKTSYVGSIVTAVGFSKGLMECAHSTG 60
DB 1 MASLGLQLVGYILGLIGLGLTLVAMLLPSWKTSYVGSIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCOESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCOESRAKDRVAVA 120
QY 121 GGVPFILGGLGRIPVAMNLHGILRDFYSPVPSDKFEIGALYLGIIISLFSLIAGII 180
DB 121 GGVPFILGGLGRIPVAMNLHGILRDFYSPVPSDKFEIGALYLGIIISLFSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNYSYSLTGYV 230
DB 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNYSYSLTGYV 230

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RESULT 15
US-10-063-512-80
; Sequence 80, Application US/10063512
; Publication No. US2003001813A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIOR APPLICATION: 2002-05-01
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 80
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-80

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Query Match 100.0%; Score 230; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASLGLQLVGYILGLIGLGLTLVAMLLPSWKTSYVGSIVTAVGFSKGLMECAHSTG 60
DB 1 MASLGLQLVGYILGLIGLGLTLVAMLLPSWKTSYVGSIVTAVGFSKGLMECAHSTG 60
QY 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCOESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGLPADIOAAMMTSSAISLACTISVGNRCCTVFCOESRAKDRVAVA 120
QY 121 GGVPFILGGLGRIPVAMNLHGILRDFYSPVPSDKFEIGALYLGIIISLFSLIAGII 180
DB 121 GGVPFILGGLGRIPVAMNLHGILRDFYSPVPSDKFEIGALYLGIIISLFSLIAGII 180
QY 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNYSYSLTGYV 230
DB 181 LCFSSCSQRNRNSNYDAYQAOPLATRSSPRGQPPKVKSEFNYSYSLTGYV 230

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Search completed: October 27, 2004, 07:50:58  
Job time : 129 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: October 27, 2004, 07:21:57 ; Search time 155 Seconds

(without alignments)  
532.308 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230  
Sequence: 1 MASLGQLVGYILGLGLG.....PGQPKVSEFNSYSLGYV 230Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*\n2: geneseqp1980s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	100.0	230	2 AAY36181	AAY36181 Human sec
2	230	100.0	230	3 AAY84609	Aay84609 A human m
3	230	100.0	230	3 AAY9378	Aay9378 Human PRO
4	230	100.0	230	4 AAB66127	Aab66127 Protein o
5	230	100.0	230	4 AAE04207	Aae04207 Human gen
6	230	100.0	230	4 AAU12417	Aau12417 Human PRO
7	230	100.0	230	4 AAU09178	Aau09178 Human PRO
8	230	100.0	230	4 AAB87565	Aab87565 Human PRO
9	230	100.0	230	4 AAB88342	Aab88342 Human mem
10	230	100.0	230	5 ABP67991	Abp67991 Human col
11	230	100.0	230	5 ABG95890	Abg95890 Human sec
12	230	100.0	230	5 ABB84912	Abb84912 Human PRO
13	230	100.0	230	5 AAU76534	Aau76534 Tuncour-as
14	230	100.0	230	5 ABG64507	Abg64507 Human alb
15	230	100.0	230	5 ABB04707	Abb04707 Human SP8
16	230	100.0	230	5 ABB95518	Abb95518 Human ang
17	230	100.0	230	6 ABO17861	Abol17861 Novel hum
18	230	100.0	230	6 ABU81115	Abu81115 Human PRO
19	230	100.0	230	6 ABU90915	Abu90915 Novel hum
20	230	100.0	230	6 ABO33974	Aboc33974 Human sec
21	230	100.0	230	6 ABU71991	Abu71991 Novel hum
22	230	100.0	230	6 ABU66815	Abu66815 Human PRO
23	230	100.0	230	6 ABU71545	Abu71545 Human sec
24	230	100.0	230	6 ABR47946	Abt47946 Human sec
25	230	100.0	230	6 ABU59896	Abu59896 Novel sec

26	230	100.0	230	6 ABU72326	Abu72326 Human PRO
27	230	100.0	230	6 ABU90999	Abu90999 Human PRO
28	230	100.0	230	6 ABO27320	Aboc27320 Human sec
29	230	100.0	230	6 ABO25086	Aboc25086 Human sec
30	230	100.0	230	6 ABR00178	Abt00178 Human gen
31	230	100.0	230	6 ABU92515	Abu92515 Human sec
32	230	100.0	230	6 ABU81185	Abu81185 Human sec
33	230	100.0	230	6 ABO53299	Aboc53299 Novel hum
34	230	100.0	230	6 ABU67091	Abu67091 Human sec
35	230	100.0	230	6 ABU98302	Abu98302 Novel hum
36	230	100.0	230	6 ABU89307	Abu89307 Novel hum
37	230	100.0	230	6 ABU82514	Abu82514 Novel hum
38	230	100.0	230	6 ABU96478	Abu96478 Human PRO
39	230	100.0	230	6 ABU72148	Abu72148 Human PRO
40	230	100.0	230	6 ADA46011	Ada46011 Novel hum
41	230	100.0	230	6 ADA76442	Ada76442 Human PRO
42	230	100.0	230	6 ADB17137	Adb17137 Human tra
43	230	100.0	230	6 ADA19092	Ada19092 Human PRO
44	230	100.0	230	6 ADA61715	Ada61715 Homo sapi
45	230	100.0	230	6 ADB19500	Adb19500 Novel hum

## ALIGNMENTS

RESULT 1  
ID AAY36181 standard; protein; 230 AA.

AC AAY36181;

DT 23-SEP-1999 (first entry)

DE Human secreted protein #53.

KM Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;  
diagnostic; gene therapy; chromosome mapping; secretion vector.

OS Homo sapiens.

PN WO9925825-A2.

PD 27-MAY-1999.

PF 13-NOV-1998; 98WO-IB001862.

PR 13-NOV-1997; 97US-0066677P.

PR 17-DEC-1997; 97US-0069957P.

PR 09-FEB-1998; 98US-0074121P.

PR 13-APR-1998; 98US-0081563P.

PR 10-AUG-1998; 98US-0096116P.

PR 04-SEP-1998; 98US-0099273P.

PA (GIST ) GENSET.

PI Bougueleret L, Duclert A, Dumas Milne Edwards J;

PS WPI: 1999-347472/29.

DR N-PSDB; AAX97865.

XX Extended cDNAs encoding secreted proteins.

XX Claim 7, Page 289, 307PP; English.

XX AAY36129-Y36222 represent novel human secreted proteins encoded by the  
extended cDNA sequences represented in AAX97813-X97906. The proteins of  
the invention have cytosolic, thrombotic and osteopathic activity. The  
extended cDNAs can be used to express secreted proteins or parts of them  
or to obtain antibodies capable of binding to the secreted proteins. They  
may also be used in diagnostic, forensic, gene therapy and chromosome  
mapping procedures. Uses also include design of expression vectors and  
secretion vectors

SQ Sequence 230 AA;  
 Query Match 100.0%; Score 230; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECATHTSG 60  
 DB 1 MASLGQLVGYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTLLGFPADIQAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITQCDIYSTLLGFPADIQAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGALYGIISLPSLIAGII 180  
 DB 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGALYGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNVYDAYQAQPLATRSSPRPGPPVKSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNVYDAYQAQPLATRSSPRPGPPVKSEFNSYSLTGYV 230

RESULT 2  
 AAY84609  
 ID AAY84609 standard; protein; 230 AA.  
 AC AAY84609;  
 XX  
 DT 25-JUL-2000 (first entry)  
 DE A human membrane associated organizational protein (HUNCT).  
 XX  
 KM Human; membrane associated organizational protein; HUNCT;  
 KM cell proliferative disorder; cancer; autoimmune disorder;  
 KM inflammatory disorder; neurological disorder; developmental disorder;  
 KM vesicle trafficking; reproductive disorder; gastrointestinal disorder;  
 KM renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;  
 KM Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;  
 KM irritable bowel syndrome; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 29  
 FT Modified-site /note= "potential phosphorylation site"  
 FT Modified-site 62  
 FT Modified-site /note= "potential phosphorylation site"  
 FT Domain 117..138  
 FT Modified-site /note= "transmembrane domain"  
 FT Modified-site 155  
 FT Modified-site /note= "potential phosphorylation site"  
 FT Domain 164..182  
 FT Modified-site /note= "transmembrane domain"  
 FT Modified-site 187  
 FT Modified-site /note= "potential phosphorylation site"  
 FT Modified-site 190  
 FT Modified-site /note= "potential glycosylation site"  
 FT Modified-site 208  
 FT Modified-site /note= "potential phosphorylation site"  
 FT Modified-site 224  
 FT Modified-site /note= "potential phosphorylation site"  
 XX  
 PN MO200018915-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 23-SEP-1999; 99WO-US022082.  
 XX  
 PR 25-SEP-1998; 98US-0155215P.  
 PR 13-OCT-1998; 98US-0155215P.  
 PR 04-MAY-1999; 99US-0172228P.  
 XX

PA (INCYTE PHARM INC.  
 XX Yue H, Lai P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;  
 XX WPI; 2000-293154/25.  
 DR N-PSDB; AAA12585.  
 DR  
 XX  
 PT Human membrane associated organizational protein and nucleic acid  
 PT sequences useful in the diagnosis, treatment and prevention of cell  
 PT proliferative associated disorders e.g. cancer, rheumatoid arthritis and  
 PT Alzheimer's disease.  
 PS Claim 1; Page 76-77; 84pp; English.  
 XX  
 CC The present sequence represents a membrane associated organizational  
 CC protein (HUNCT). HUNCT is used for the diagnosis, treatment and  
 CC prevention of cell proliferative disorders including cancer and  
 CC autoimmune/inflammatory, neurological, developmental, vesicle  
 CC trafficking, reproductive, gastrointestinal and renal disorders. These  
 CC disorders may include atherosclerosis, leukaemia, allergies, rheumatoid  
 CC arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects,  
 CC renal failure and irritable bowel syndrome. A vector expressing HUNCT,  
 CC and an agonist of HUNCT can be used to treat or prevent a disorder  
 CC associated with decreased expression or activity of HUNCT. An antagonist  
 CC of HUNCT or a vector expressing the complement of a polynucleotide  
 CC encoding HUNCT can be used to treat or prevent a disorder associated with  
 CC increased expression or activity of HUNCT. Antibodies which bind HUNCT  
 CC can be used for diagnosis of disorders associated with HUNCT expression  
 CC or to monitor patients being treated with HUNCT, agonists, antagonists or  
 CC inhibitors of HUNCT. Assays are preferably carried out on body fluids  
 CC from a patient using radioimmunoassay, enzyme linked immunosorbent assays  
 CC or fluorescent activated cell sorting assays. Polynucleotides encoding  
 CC HUNCT are also used in hybridisation assays to determine absence,  
 CC presence or excess expression of HUNCT and to monitor regulation of HUNCT  
 CC levels during disease therapy  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 230; DB 3; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECATHTSG 60  
 DB 1 MASLGQLVGYIIIGLGLGLTLVAMLLPSWKTSYVGASIVTVAVGSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTLLGFPADIQAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITQCDIYSTLLGFPADIQAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGALYGIISLPSLIAGII 180  
 DB 121 GGVFFILGILGFIPIVAMNHLGILRDFSPPLVPSDKMFEIGALYGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNVYDAYQAQPLATRSSPRPGPPVKSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNVYDAYQAQPLATRSSPRPGPPVKSEFNSYSLTGYV 230

RESULT 3  
 AAY9378  
 ID AAY9378 standard; protein; 230 AA.  
 AC AAY9378;  
 XX  
 DT 06-AUG-2000 (first entry)  
 DE Human PRO1356 (UNQ705) amino acid sequence SEQ ID NO:134.  
 XX  
 KM Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 KM transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
 XX  
 OS Homo sapiens.

XX WO200012708-A2.  
 XX 09-MAR-2000.  
 XX 01-SEP-1999; 99WO-US020111.  
 XX 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.  
 PR 09-SEP-1998; 98US-0099596P.  
 PR 09-SEP-1998; 98US-0099598P.  
 PR 09-SEP-1998; 98US-0099602P.  
 PR 09-SEP-1998; 98US-0099642P.  
 PR 10-SEP-1998; 98US-0099741P.  
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 PR 10-SEP-1998; 98US-0099763P.  
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 PR 10-SEP-1998; 98US-0099816P.  
 PR 15-SEP-1998; 98US-0100385P.  
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 PR 15-SEP-1998; 98US-0100390P.  
 PR 16-SEP-1998; 98US-0100584P.  
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 PR 18-SEP-1998; 98US-0100848P.  
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 PR 03-NOV-1998; 98US-0106905P.  
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 PR 17-NOV-1998; 98US-0108802P.  
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 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX (GETH ) GENENTECH INC.  
 PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;  
 PI WPI; 2000-237871/20.  
 XX N-PSDB; AAA37060.  
 DR New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 XX PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX Claim 12; Fig 76; 773pp; English.  
 PS AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 XX receptor or secreted PRO polypeptides given in AAY9340 to AAY93462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of

CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding them have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAs3145 to AAs3730 represent PCR  
CC primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 3; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITCCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITCCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180  
DB 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 4  
AAB66127  
ID AAB66127 standard; protein; 230 AA.

AC AAB66127;

DT 02-APR-2001 (first entry)

XX Protein of the invention #39.

XX Secreted; transmembrane; gene therapy.

XX Unidentified.

XX WO200078961-A1.

XX 28-DEC-2000.

XX 18-FEB-2000; 2000WO-US0004342.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 29-OCT-1999; 99US-0162506P.

XX 30-OCT-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028551.

XX 16-DEC-1999; 99WO-US030095.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
XX Geo W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
XX Williams PM, Wood WI;  
XX WPI; 2001-071395/08.  
XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
XX PT useful as hybridization probes, in chromosome and gene mapping and gene  
XX therapy.

XX Claim 1; Fig 78; 787pg; English.

XX The present invention relates to secreted and transmembrane proteins.  
XX These proteins and the DNA encoding them may be used as hybridization  
XX probes, in chromosome and gene mapping and in the generation of anti-  
XX sense RNA and DNA. They may also be used to generate either  
XX transgenic animals or knockout animals which are in turn useful for  
XX development and screening of therapeutically useful reagents. The nucleic  
XX acids may also be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGQLVGYIIGLGLGLTLVAMLLPSWKTSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITCCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITCCDIYSTLLGLPADIOAAMMTSSAISLACTISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180  
DB 121 GGVFTLLGLGLFIPVAMNHLGILRDFYSPVLPDSMKFEIGEALYIGIISLFSLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPPRGQPPVKSEFNSYSLTGYV 230

RESULT 5  
AAB04207

ID AAB04207 standard; protein; 230 AA.

AC AAB04207;

DT 09-AUG-2001 (first entry)

XX Human gene 10 encoded secreted protein HRP183, SEQ ID NO:62.

XX Human; secreted protein; proliferative disorder; cancer; tumour;  
XX foetal abnormality; developmental abnormality; haematopoietic disorder;  
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
XX inflammation; allergy; neurological disorder; Alzheimer's disease;  
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
XX cardiovascular disorder; angiotensin disorder; kidney disorder;  
XX gastrointestinal disorder; pregnancy-related disorder; gene therapy;  
XX endocrine disorder; infection; wound healing; vulnery; cell culture;  
XX chemotaxis; food additive; binding partner identification.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24 /label= signal\_peptide

FT Protein 25..230 /note="Mature secreted protein"

XX WO200136432-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US031162.

XX 19-NOV-1999; 99US-0166415P.

XX 30-JUN-2000; 2000US-0215136P.

XX (HUMA-) HUMAN GENOME SCI INC.



CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of a peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
DB 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITCCDIYSTLGLPADIQAAQAMWVTSSAISLACITISVVMRCCTVQCSRRAKDRVAVA 120  
DB 61 ITCCDIYSTLGLPADIQAAQAMWVTSSAISLACITISVVMRCCTVQCSRRAKDRVAVA 120  
QY 121 GGVFFIIGLGLFIPVAMNHLGILRDFYSPVDPMSKEFGEALYGIISLSFLAGIT 180  
DB 121 GGVFFIIGLGLFIPVAMNHLGILRDFYSPVDPMSKEFGEALYGIISLSFLAGIT 180  
QY 181 LCRSCSSQRNRNRYNDAYQAPLATRSSPRGQPPKXSEFNYSLTGYV 230  
DB 181 LCRSCSSQRNRNRYNDAYQAPLATRSSPRGQPPKXSEFNYSLTGYV 230

#### RESULT 7

AAU09178 ID AAU09178 standard; protein; 230 AA.

AC AAU09178;

XX 16-JAN-2002 (first entry)

XX Human PRO1356 polypeptide.

XX Human; PRO1356; clone DNA64886-1601; immune-related disorder;  
XX inflammatory disorder; infectious disorder; immunodeficiency disorder;  
XX autoimmune disorder; renal disease; demyelinating disease; skin disease;  
XX neoplasia; transplantation associated disease; immunosuppressive;  
XX anti-inflammatory; antidiabetic; antidiabetic.

OS Homo sapiens.

XX Location/Qualifiers

FT Peptide 1..24 /label= Signal\_peptide

FT Modified-site 17..23 /note= "N-myristoylation site"

FT Modified-site 20..26 /note= "N-myristoylation site"

FT Protein 25..230 /label= Mature\_PRO1356\_polypeptide

FT Region 46..60 /note= "Also found in PMP-22, EMP and MP20 family proteins"

FT Modified-site 60..66 /note= "N-myristoylation site"

FT Domain 82..102

FT /label= Transmembrane\_domain  
FT 101..107 /note= "N-myristoylation site"  
FT Domain 117..140 /label= Transmembrane\_domain  
FT Modified-site 128..134 /note= "N-myristoylation site"  
FT Domain 153..182 /label= Transmembrane\_domain  
FT Modified-site 167..173 /note= "N-myristoylation site"  
FT Modified-site 178..184 /note= "N-myristoylation site"  
FT Modified-site 190..194 /note= "N-glycosylation site"  
FT Modified-site 216..225 /note= "Tyrosine kinase phosphorylation site"

XX WO200166740-A2.

XX 13-SEP-2001.

PF 01-MAR-2001; 2001MO-US006666.

XX 03-MAR-2000; 2000US-0187202P.  
XX 21-MAR-2000; 2000US-0191015P.  
XX 30-MAY-2000; 2000MO-US014941.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 24-AUG-2000; 2000MO-US023328.  
XX 01-DEC-2000; 2000MO-US032678.

XX (GENTH ) GENENTECH INC.

XX Eaton DU, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
PI Tuma D, Watanabe CK, Wood WI, Zhang Z;

XX WPI, 2001-625876/72.

DR N-PSDB; AAS15360.

XX Nucleic acids encoding PRO polypeptides, useful for detecting and  
PT treating immune related diseases and disorders in mammals including  
PT autoimmune diseases, inflammatory diseases and asthma.

XX Claim 10; Fig 2; 122pp; English.

XX The present invention relates to the isolation of 9 novel human PRO  
CC polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.  
CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,  
CC PRO3151, PRO4322, PRO3964, PRO10008 and PRO19598. The cDNA sequences  
CC encoding these PRO polypeptides have been designated as clones DNA64886-  
CC 1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA92223-2567,  
CC DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g.  
CC vaccines) containing PRO polypeptides and methods of using these  
CC compositions are useful in the treatment and diagnosis of immune-related  
CC disorders. Such disorders include immune-mediated inflammatory disorders  
CC (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g.  
CC diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis),  
CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g.  
CC rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis),  
CC demyelinating diseases of the peripheral or central nervous system (e.g.  
CC Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact  
CC dermatitis), neoplasias and transplantation associated diseases. The  
CC polynucleotide sequences of the invention may be used in gene therapy.  
CC AAU09178-AAU09186 represent the novel human PRO polypeptides of the  
XX invention

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60



```
DB 1 MASLGLQVGYIIGLGLGTLVAMLLPSWKTSSYVAGSIIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGHPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGHPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVPFLLGLGLGHPVAMNHLGILRDFYSPVLPDMSKFEIGELALYIGIISLFSLLAGII 180
DB 121 GGVPFLLGLGLGHPVAMNHLGILRDFYSPVLPDMSKFEIGELALYIGIISLFSLLAGII 180
QY 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPPGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPPGQPPKVKSEFNSYSLTGYV 230

RESULT 8
AAB87565
ID AAB87565 standard; protein; 230 AA.
XX
AC AAB87565;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1356.
XX
KM Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000MO-US023328.
XX
PR 01-SEP-1999; 99MO-US020111.
PR 15-SEP-1999; 99MO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175461P.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 01-MAR-2000; 2000MO-US005601.
PR 03-MAR-2000; 2000US-0187282P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000MO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000MO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Mactanabe CK, Wood WI,
XX WPI; 2001-183260/18.
XX DR N-PSDB; AAF92097.
XX
XX Bighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
XX Claim 12; Fig 80; 278bp; English.
XX
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
```

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CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 230 AA;
QY 100.0%; Score 230; DB 4; Length 230;
DB Best Local Similarity 100.0%; Pred.No.3.9e-210; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;
QY 1 MASLGLQVGYIIGLGLGTLVAMLLPSWKTSSYVAGSIIVTAVGFSKGLMECATHTSG 60
DB 1 MASLGLQVGYIIGLGLGTLVAMLLPSWKTSSYVAGSIIVTAVGFSKGLMECATHTSG 60
QY 61 ITQCDIYSTLLGHPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKDRVAVA 120
DB 61 ITQCDIYSTLLGHPADIQAAQAMMTSSAISLACIIISVGMCTVFCQESRAKDRVAVA 120
QY 121 GGVPFLLGLGLGHPVAMNHLGILRDFYSPVLPDMSKFEIGELALYIGIISLFSLLAGII 180
DB 121 GGVPFLLGLGLGHPVAMNHLGILRDFYSPVLPDMSKFEIGELALYIGIISLFSLLAGII 180
QY 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPPGQPPKVKSEFNSYSLTGYV 230
DB 181 LCFSSCSQRNRSNYYDAYQAQPLATRSSPPGQPPKVKSEFNSYSLTGYV 230

RESULT 9
AAB88342
ID AAB88342 standard; protein; 230 AA.
XX
AC AAB88342;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSRC0059.
XX
KM Human; secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Oca T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
PI WPI; 2001-093989/11.
XX DR N-PSDB; AAF93769.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
XX Claim 1; SEQ ID NO 52; 609pp + Sequence Listing; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
```

CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
CC and quantitate the presence of similar nucleic acid sequences in samples.  
CC They may also be used to study the expression and function of secretory  
CC proteins/membrane polypeptides and their role in metabolism. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC against them and in assays to identify modulators (agonists and  
CC antagonists) of expression and activity. The antibodies and antagonists  
CC may also be used as therapeutic agents to down regulate expression and  
CC activity. The antibodies may also be used as diagnostic agents for  
CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
CC treated include rheumatoid arthritis and diabetes

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210; Mismatches 0; Gaps 0;

Matches 230; Conservative 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLPIPAVMNHGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180  
DB 121 GGVFFILGLGLPIPAVMNHGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 10  
ABP67991

ID ABP67991 standard; protein; 230 AA.

XX ABP67991;

XX 13-DEC-2002 (first entry)

XX Human colon cancer related polypeptide SEQ ID NO 2590.

XX Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine.

XX Homo sapiens.

XX WO200258534-A2.

XX 01-AUG-2002.

XX 16-NOV-2001; 2001WO-US043704.

XX 20-NOV-2000; 2000US-0252222P.

XX 06-FEB-2001; 2001US-0267011P.

XX 28-MAR-2001; 2001US-0279670P.

XX 10-JUL-2001; 2001US-0304037P.

XX (CORI-) CORIXA CORP.

XX Stolk JA, Xu J, Chenault RA, Meagher MJ, Secretist H, King GE;

XX WPI; 2002-608400/65.

XX N-PSDB; ABV89278.

XX New isolated tumor colon polynucleotide and polypeptide, useful for the  
XX diagnosis, prevention and/or treatment of cancer, in particular colon  
XX cancer.

XX Claim 2; SEQ ID NO 2590; 266pp + Sequence Listing; English.

XX The invention relates to a human colon tumour expressed polynucleotide  
CC (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of  
CC 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)  
CC complements of (i); (iii) at least 20 contiguous residues of (i); (iv)  
CC sequences that hybridize to (i), under moderately stringent conditions;  
CC (v) sequences having at least 75% or 90% identity to (i); or (vi)  
CC degenerate variants of (i). The compositions and methods of the present  
CC invention are useful for the diagnosis, prevention and/or treatment of  
CC cancer, particularly colon cancer. (i) can be used in gene therapy and  
CC (i) and (ii) are useful in pharmaceutical compositions such as vaccines.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210; Mismatches 0; Gaps 0;

Matches 230; Conservative 0; Indels 0; Gaps 0;

QY 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
DB 1 MASLGLQVGYIIGLGLGLTVAMLLPSWKTSSYVGASIVTAVGSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120  
DB 61 ITQCDIYSTLLGLPADIOAAQAMWVTSASISLACIISVGMKCTVFCQESRAKDRVAVA 120  
QY 121 GGVFFILGLGLPIPAVMNHGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180  
DB 121 GGVFFILGLGLPIPAVMNHGILRDYSPVLDPSMKFEIGELALYIGIISLSFLIAGII 180  
QY 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230  
DB 181 LCFSSCSQRNRSNYDAYOAOPLATRSSPRPGQPPVKSEFNSYSLTGYV 230

RESULT 11  
ABG95890

ID ABG95890 standard; protein; 230 AA.

XX ABG95890;

XX 10-DEC-2002 (first entry)

XX Human secreted/transmembrane protein PRO1356.

XX Human; secreted protein; transmembrane protein; anti-rheumatic;  
XX antiarthritic; osteopathic; sports-related joint problem;  
XX articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

XX US2002119130-A1.

XX 29-AUG-2002.

XX 06-DEC-2001; 2001US-00006867.

XX 29-OCT-1997; 97US-0063435P.

XX 29-OCT-1997; 97US-0064215P.

XX 29-APR-1998; 98US-0082797P.

XX 29-APR-1998; 98US-0083495P.

XX 15-MAY-1998; 98US-0085579P.

XX 02-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088029P.

XX 10-JUN-1998; 98US-0088030P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088740P.

XX 10-JUN-1998; 98US-0088811P.

XX 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 19-JUN-1998; 98US-0089552P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 25-JUN-1998; 98US-0090688P.  
 PR 25-JUN-1998; 98US-0090686P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 10-SEP-1998; 98US-0099815P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100652P.  
 PR 16-SEP-1998; 98US-0100653P.  
 PR 17-SEP-1998; 98US-0100683P.  
 PR 17-SEP-1998; 98US-0100684P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 22-SEP-1998; 98US-0101279P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 24-SEP-1998; 98US-0101916P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 08-MAR-1999; 99US-05005028.  
 PR 14-MAY-1999; 99US-05010733.  
 PR 02-JUN-1999; 99US-05012252.  
 PR 01-SEP-1999; 99US-05020111.  
 PR 15-SEP-1999; 99US-05021090.  
 PR 15-SEP-1999; 99US-05021194.  
 PR 22-DEC-1999; 99US-05030720.  
 PR 18-FEB-2000; 2000US-05004341.  
 PR 18-FEB-2000; 2000US-05004342.  
 PR 22-FEB-2000; 2000US-05004414.  
 PR 01-MAR-2000; 2000US-05005601.  
 PR 01-MAR-2000; 2000US-05008439.  
 PR 30-MAR-2000; 2000US-05014042.  
 PR 02-JUN-2000; 2000US-05015264.  
 PR 23-AUG-2000; 2000US-05023522.  
 PR 24-AUG-2000; 2000US-05023328.  
 PR 10-NOV-2000; 2000US-05030873.  
 PR 01-DEC-2000; 2000US-05032378.  
 PR 20-DEC-2000; 2000US-05034356.  
 PR 28-FEB-2001; 2001US-05006520.  
 PR 01-MAR-2001; 2001US-05006566.  
 PR 30-MAY-2001; 2001US-05017443.  
 PR 01-JUN-2001; 2001US-05017800.  
 PR 20-JUN-2001; 2001US-05019692.  
 PR 29-JUN-2001; 2001US-05021066.  
 PR 09-JUL-2001; 2001US-05021735.  
 XX  
 PA (GERTH ) GENENTECH INC.  
 XX  
 PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
 XX Grimaldi JC, Gurney AJ, Watanabe CK, Wood WI,  
 DR WPI; 2002-731348/79.  
 XX N-PSDB; ABS74417.

PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating sports-related  
 PT joint problems, osteoarthritis or rheumatoid arthritis.  
 PS  
 XX Claim 20; Fig 80; 399pp; English.  
 XX  
 PR The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing as  
 CC AAG35851-ABG95934 or their associated signal peptide, or a sequence of an  
 CC extracellular domain of the proteins with their associated signal peptide  
 CC or lacking its associated signal peptide. Also included are the nucleic  
 CC acids encoding the proteins, vectors, host cells, fusion proteins and  
 CC antibodies which specifically bind to the proteins. The proteins are  
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
 CC suspected of containing an A, B, C or D polypeptide, by contacting the  
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide  
 CC conjugate in the sample, where the formation of the conjugate is  
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
 CC PRO10066 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
 CC H or I polypeptide is labeled with a detectable label or is attached to a  
 CC solid support. The proteins are useful for linking a bioactive molecule  
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
 CC or I, or antibodies against them are useful for modulating a biological  
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
 CC identifying agonists or antagonists, for the preparation of a medicament  
 CC useful in the treatment of a condition which is responsive to the  
 CC proteins, as molecular weight markers for protein electrophoresis  
 CC purposes, and as therapeutic agents for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis. Nucleic acids encoding the proteins are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
 CC generate transgenic or knockout animals which are useful in the  
 CC development and screening of therapeutic useful reagents, for chromosome  
 CC identification, and in gene therapy. The antibody is useful as a  
 CC therapeutic agent, in a diagnostic assay and for affinity purification of  
 CC the protein from recombinant cell culture natural sources. The present  
 CC sequence represents a novel secreted or transmembrane protein of the  
 CC invention  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 230; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3,9e-210; Indels 0; Gaps 0;  
 Matches 230; Conservative 0; Mismatches 0;  
 QY 1 MASIGLVGYITIGLGLTGLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECAHTSTG 60  
 Db 1 MASIGLVGYITIGLGLTGLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECAHTSTG 60  
 QY 61 ITQCDIVSTLLGLPADIOAAMVTSATSIACIIISVVGKCTVFCQSSRAKDRVVA 120  
 Db 61 ITQCDIVSTLLGLPADIOAAMVTSATSIACIIISVVGKCTVFCQSSRAKDRVVA 120  
 QY 121 GGVFFITIGLLGFIPIVAMNHLGILRDFPSPLVPDSMKFEIGELALYIGITISLSLGIIT 180  
 Db 121 GGVFFITIGLLGFIPIVAMNHLGILRDFPSPLVPDSMKFEIGELALYIGITISLSLGIIT 180  
 QY 181 LCFSCSSQRNRSNYDYAYQAPLATRSSPRPGQPPKVSSEFNSYSLTGYV 230  
 Db 181 LCFSCSSQRNRSNYDYAYQAPLATRSSPRPGQPPKVSSEFNSYSLTGYV 230  
 RESULT 12  
 ABB84912

ID ABB84912 standard; protein; 230 AA.  
 XX ABB84912;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Human PRO1356 protein sequence SEQ ID NO:192.  
 KM Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
 KM vlneryary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KM age-related macular degeneration; arterial restenosis; angina;  
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KM wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.  
 PN WC020020690-A2.  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001MO-US019692.  
 XX  
 PR 23-JUN-2000; 2000US-0213637P.  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 17-AUG-2000; 2000US-00643657.  
 PR 23-AUG-2000; 2000MO-US023522.  
 PR 07-SEP-2000; 2000MO-US030952.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 10-NOV-2000; 2000MO-US030873.  
 PR 01-DEC-2000; 2000MO-US032578.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000MO-US034556.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001MO-US006520.  
 PR 01-MAR-2001; 2001MO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 12-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 30-MAY-2001; 2001MO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001MO-US017443.  
 PR 01-JUN-2001; 2001MO-US017800.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,  
 XX  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88167.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX  
 PS Claim 11; Fig 192; 565bp; English.  
 CC ABB88072 to ABB88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,  
 CC antiangiogenic, hypotensive, vlneryary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABB88259 to ABB88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 230 AA;  
 Query Match 100.0%; Score 230; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASLGQLVGYITGLGLGLTVMALLPSWKTSSYGAIVTVAVGSKLMECAHSTG 60  
 DB 1 MASLGQLVGYITGLGLGLTVMALLPSWKTSSYGAIVTVAVGSKLMECAHSTG 60  
 QY 61 ITQCDYSTLGLPADIOAQAAMWTSASISLACIISVGNRCYFCQESRAKORVAVA 120  
 DB 61 ITQCDYSTLGLPADIOAQAAMWTSASISLACIISVGNRCYFCQESRAKORVAVA 120  
 QY 121 GGVFFILGILGRIPIVAMNHGILRDYSPVLPDSMKFIEGALYGIISLPSLIAGII 180  
 DB 121 GGVFFILGILGRIPIVAMNHGILRDYSPVLPDSMKFIEGALYGIISLPSLIAGII 180  
 QY 181 LCFSCSSQRNRNRYDVAQAOPLATSSPRPQPPVKSEFNSYSILTV 230  
 DB 181 LCFSCSSQRNRNRYDVAQAOPLATSSPRPQPPVKSEFNSYSILTV 230  
 RESULT 13  
 ID AAB76534 standard; protein; 230 AA.  
 XX  
 XX AAB76534;  
 AC  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Tumour-associated antigenic target protein, TAT134.  
 XX  
 KM TAT134; Tumour-associated Antigenic Target; tumour; breast cancer;  
 KM colorectal cancer; lung cancer; ovarian cancer;  
 KM central nervous system cancer; liver cancer; bladder cancer; melanoma;  
 KM pancreatic cancer; leukaemia; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT Region /note= "Signal sequence"  
 FT Modified-site 4..181  
 FT Modified-site /note= "BMP-32/EMP/MP30/Claudin family (not defined)"  
 FT Modified-site 17..22  
 FT Modified-site /note= "N-myristoylation site"  
 FT Modified-site 20..25  
 FT Protein /note= "N-myristoylation site"  
 FT Protein 25..230  
 FT Modified-site /note= "Mature TAT134"  
 FT Modified-site 60..65  
 FT Modified-site /note= "N-myristoylation site"  
 FT Domain 82..102  
 FT /note= "Transmembrane domain"

FT Modified-site 101..106  
 FT /note= "N-myristoylation site"  
 FT Domain 120..140  
 FT /note= "Transmembrane domain"  
 FT Modified-site 128..133  
 FT /note= "N-myristoylation site"  
 FT Domain 160..180  
 FT /note= "Transmembrane domain"  
 FT Modified-site 167..172  
 FT /note= "N-myristoylation site"  
 FT Modified-site 178..183  
 FT /note= "N-myristoylation site"  
 FT Modified-site 190..193  
 FT /note= "Aen is N-glycosylated"  
 FT Modified-site 216..224  
 FT /note= "Tyrosine kinase phosphorylation site"  
 PN WO200216429-A2.  
 PD 28-FEB-2002.  
 PF 22-JUN-2001; 2001WO-US020118.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 26-SEP-2000; 2000US-0235451P.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PA (GETH ) GENENTECH INC.  
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V,  
 PI Wood WI, Wu TD, Zhang Z;  
 XX WPI; 2002-280917/32.  
 DR N-PSB; ABK11089.  
 XX  
 PT Novel isolated tumor-associated antigenic target polypeptides which are  
 PT useful as targets for cancer therapy and diagnosis in mammals.  
 PS  
 PS Claim 12; Fig 6; 121pp; English.  
 XX  
 XX The invention relates to an isolated tumour-associated antigenic target  
 CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the  
 CC polynucleotides (II) encoding them. (II) is useful for diagnosing the  
 CC presence of a tumour in a mammal, where the level of expression of (II)  
 CC is indicative on the presence of tumour in the mammal from which the test  
 CC sample was obtained. Antibody to (I) is useful for killing a cancer cell,  
 CC (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,  
 CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a  
 CC liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a  
 CC melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides  
 CC hybridising to (II) are useful as diagnostic probes, antisense  
 CC oligonucleotide probes or for encoding fragments of full length TAT  
 CC polypeptide. (II) is also useful in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA probes, for constructing  
 CC hybridisation probes for mapping the gene encoding TAT and for genetic  
 CC analysis of individuals with genetic disorders. (II) is also useful for  
 CC generating either transgenic animals or knockout animals, and in gene  
 CC therapy. The TAT polypeptides and nucleic acids may also be used for  
 CC tissue typing and the TAT polypeptides are useful for screening compounds  
 CC that mimic the TAT polypeptide (agonists) or prevent the effect of TAT  
 CC polypeptide (antagonists). The antibody is useful for staging TAT  
 CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT  
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide  
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or  
 CC Western blot. The antibodies are also useful for treating a TAT-  
 CC expressing cancer or alleviating one or more symptoms of cancer in a  
 CC mammal. The present sequence represents the amino acid sequence of TAT134  
 XX  
 XX Sequence 230 AA;  
 SQ  
 Query Match 100.0%; Score 230; DB 5; Length 230;

Best Local Similarity 100.0%; Pred. No. 3.9e-210; Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASIGOLVGYILGLGLGLTVAAMLPSWKTSYVGAISIVAVGSKGLMECAHTSTG 60  
 DB 1 MASIGOLVGYILGLGLGLTVAAMLPSWKTSYVGAISIVAVGSKGLMECAHTSTG 60  
 QY 61 ITCCDYSYTLGLPADIOAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITCCDYSYTLGLPADIOAAQAMWVTSSAISLACIIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVPFLIGLGLPIPVAMNHLGIRDPYSPVVDNSKFEIGELLYIGIISLSPLAGII 180  
 DB 121 GGVPFLIGLGLPIPVAMNHLGIRDPYSPVVDNSKFEIGELLYIGIISLSPLAGII 180  
 QY 181 LCFSCSSQRNRSMNYDAYOAOPLATSSPPGQPPVKSEFNSYSLTGYY 230  
 DB 181 LCFSCSSQRNRSMNYDAYOAOPLATSSPPGQPPVKSEFNSYSLTGYY 230  
 RESULT 14  
 ID ABG64507 standard; protein; 230 AA.  
 XX  
 AC ABG64507;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human albumin fusion protein #1182.  
 XX  
 XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW hematopoietic disorder; neural disorder; connective disorder;  
 KW cytostatic; antineoplastic; antiinflammatory; anticancer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antichratic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200177137-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US011988.  
 XX  
 XX 12-APR-2000; 2000US-0229358P.  
 PR 25-APR-2000; 2000US-019384P.  
 PR 21-DEC-2000; 2000US-0256931P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Haseltine WA;  
 XX  
 XX WPI; 2002-010886/01.  
 DR  
 PT New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein.  
 PS  
 PS Claim 1; Page 1277-1278; 2102pp; English.  
 XX  
 XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA), also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or disorder  
 CC that may be modulated by therapeutic protein X. The albumin extends the  
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo  
 CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC hematopoietic disorders, neural disorders (e.g. Alzheimer's,

CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC Schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX  
 SQ Sequence 230 AA;

Query Match 100.0%; Score 230; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVLGVYIIGLGLGLTLVAMLLPSWKTSYVGSIVTVAVGFSKGLMECATHTSTG 60  
 DB 1 MASLGLQVLGVYIIGLGLGLTLVAMLLPSWKTSYVGSIVTVAVGFSKGLMECATHTSTG 60  
 QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFIIGLGLGFIPVAMNHLGILRDPYSPVPSMKFEIGEALYIGIISLPSLIAGII 180  
 DB 121 GGVFFIIGLGLGFIPVAMNHLGILRDPYSPVPSMKFEIGEALYIGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNYDYAQAOPLATRSSPRPGOPPKVSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNYDYAQAOPLATRSSPRPGOPPKVSEFNSYSLTGYV 230

RESULT 15

ABB04707  
 ID ABB04707 standard; protein; 230 AA.

AC ABB04707;

DT 11-MAR-2002 (first entry)

DE Human SP82 protein SEQ ID NO:2.

XX Human; SP82; cancer suppression.

XX Homo sapiens.

OS CN1313315-A.

XX 19-SEP-2001.

XX 13-MAR-2000; 2000CN-00111989.

XX 13-MAR-2000; 2000CN-00111989.

PA (SHAN-) SHANGHAI INST ONCOLOGY.

PI Gu J, Yang S;

DR WPI; 2002-042193/06.

DR N-PSDB; ABA04424.

XX New human protein able to suppress growth of cancer cells and its  
 PT encoding polynucleotide sequence.

XX Claim 1; Page 12 (Disclosure); 42pp; Chinese.

CC The present sequence represents human SP82 protein, which has cancer-  
 CC suppressing activity. The present invention also describes a method for  
 CC the preparation of the protein by recombination, and the application of  
 CC the protein in treating diseases such as cancer

XX Sequence 230 AA;

Query Match 100.0%; Score 230; DB 5; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLQVLGVYIIGLGLGLTLVAMLLPSWKTSYVGSIVTVAVGFSKGLMECATHTSTG 60

DB 1 MASLGLQVLGVYIIGLGLGLTLVAMLLPSWKTSYVGSIVTVAVGFSKGLMECATHTSTG 60  
 QY 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 DB 61 ITQCDIYSTLLGLPADIQAAQAMMTSSAISLACIISVGMKCTVFCQESRAKDRVAVA 120  
 QY 121 GGVFFIIGLGLGFIPVAMNHLGILRDPYSPVPSMKFEIGEALYIGIISLPSLIAGII 180  
 DB 121 GGVFFIIGLGLGFIPVAMNHLGILRDPYSPVPSMKFEIGEALYIGIISLPSLIAGII 180  
 QY 181 LCFSSCSQRNRSNYDYAQAOPLATRSSPRPGOPPKVSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNRSNYDYAQAOPLATRSSPRPGOPPKVSEFNSYSLTGYV 230

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OM protein - protein search, using SW model

Run on: October 27, 2004, 07:30:58 ; Search time 41 Seconds  
(without alignments)  
372.028 Million cell updates/sec

Title: US-09-787-677a-3

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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230	100.0	230	US-09-663-600A-186	Sequence 186, App
2	230	100.0	230	US-10-140-002-492	Sequence 492, App
3	127	55.2	230	US-09-663-600A-92	Sequence 92, Appl
4	38	16.5	42	US-09-282-029A-7	Sequence 7, Appl
5	38	16.5	42	US-09-185-908-7	Sequence 7, Appl
6	9	3.9	208	US-09-252-991A-22641	Sequence 22641, A
7	8	3.5	31	US-08-525-539A-34	Sequence 34, Appl
8	3.5	58	4	US-09-275-252A-32	Sequence 32, Appl
9	3.5	138	4	US-09-252-991A-16828	Sequence 16828, A
10	8	3.5	335	US-09-248-796A-17661	Sequence 17661, A
11	8	3.5	341	US-09-190-965-3	Sequence 3, Appl
12	8	3.5	341	US-09-470-253-3	Sequence 3, Appl
13	8	3.5	487	US-09-252-991A-28079	Sequence 28079, A
14	8	3.5	673	US-09-091-725-13	Sequence 13, Appl
15	8	3.5	673	US-09-091-725-19	Sequence 19, Appl
16	8	3.5	673	US-09-091-725-23	Sequence 23, Appl
17	8	3.5	1196	US-09-275-252A-9	Sequence 9, Appl
18	8	3.5	4550	US-08-804-227C-8	Sequence 8, Appl
19	8	3.5	4550	US-08-804-198-2	Sequence 2, Appl
20	7	3.0	8	US-09-282-029A-131	Sequence 131, App
21	7	3.0	8	US-09-185-908-131	Sequence 131, App
22	7	3.0	30	US-09-282-029A-473	Sequence 473, App
23	7	3.0	31	US-08-525-539A-32	Sequence 32, Appl
24	7	3.0	37	US-08-789-333F-16	Sequence 16, Appl
25	7	3.0	37	US-09-133-944-16	Sequence 16, Appl
26	7	3.0	37	US-09-208-827-17	Sequence 17, Appl
27	7	3.0	37	US-08-787-738B-16	Sequence 16, Appl

28	7	3.0	37	4	US-09-157-748-19	Sequence 19, Appl
29	7	3.0	37	4	US-09-800-170-69	Sequence 69, Appl
30	7	3.0	37	4	US-10-043-074-17	Sequence 17, Appl
31	7	3.0	37	4	US-09-285-912A-79	Sequence 79, Appl
32	7	3.0	37	4	US-09-578-030-20	Sequence 20, Appl
33	7	3.0	37	4	US-09-516-940-16	Sequence 16, Appl
34	7	3.0	42	1	US-08-004-492-4	Sequence 4, Appl
35	7	3.0	42	1	US-08-004-492-7	Sequence 7, Appl
36	7	3.0	67	4	US-09-543-681A-7721	Sequence 7721, Ap
37	7	3.0	93	4	US-09-489-039A-7356	Sequence 7356, Ap
38	7	3.0	93	4	US-09-489-039A-11691	Sequence 11691, A
39	7	3.0	97	4	US-09-519-878-6	Sequence 6, Appl
40	7	3.0	102	1	US-08-282-951-2	Sequence 2, Appl
41	7	3.0	105	4	US-09-107-532A-5500	Sequence 5500, Ap
42	7	3.0	110	1	US-08-017-570-2	Sequence 2, Appl
43	7	3.0	110	1	US-08-471-426-2	Sequence 2, Appl
44	7	3.0	110	3	US-09-672-609-13	Sequence 13, Appl
45	7	3.0	110	4	US-09-025-403A-13	Sequence 13, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-663-600A-186
Sequence 186, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
TITLE OF INVENTION: Bouguerelet, Lydie
FILE REFERENCE: 31. US3. CIP
CURRENT APPLICATION NUMBER: US/09/663, 600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191, 997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066, 677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069, 957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074, 121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081, 563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096, 116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099, 273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 186
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SIGNAL
LOCATION: -24...-1
US-09-663-600A-186
Query Match 100.0%; Score 230; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.7e-208;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASLGLQVGVYIIGLGLTGLVAMLLPSWKTSYVGASTVAVGFSKGLMECAHTSTG 60
Db 1 MASLGLQVGVYIIGLGLTGLVAMLLPSWKTSYVGASTVAVGFSKGLMECAHTSTG 60
QY 61 ITCCDYSYTLGLPADIQAQAAMMTSSAITSACTIISVGMKCTVPCOSSRAKDVAVA 120
Db 61 ITCCDYSYTLGLPADIQAQAAMMTSSAITSACTIISVGMKCTVPCOSSRAKDVAVA 120
QY 121 GGVFFILGLGLPFPVAMNHLGILRDFYSPPLVDMSKMEIGALYIGIISLPSLIAGII 180
```



Db 121 GGVEFIIIGLGFIPVAMNHLGILRDFYSPVPDSMKFEIGEAALYDIIISLPSLGIIT 180  
QY 181 LCFSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYSILGYV 230  
Db 181 LCFSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYSILGYV 230

## RESULT 2

US-10-140-002-492  
Sequence 492, Application US/10140002  
Patent No. 6725730  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS  
FILE REFERENCE: P330R1C59  
CURRENT APPLICATION NUMBER: US/10/140,002  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 492  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-140-002-492

Query Match 100.0%; Score 230; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 9.7e-208;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASIGLOLVGYIILGLIGLITVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
Db 1 MASIGLOLVGYIILGLIGLITVAMLLPSWKTSSYVGASIVTAVGFSKGLMECATHTSG 60  
QY 61 ITQCDIYSTLLGLPADIOAAQAMMVTSSAISLACIISVGMRCCTVCOESRAKORVAVA 120  
Db 61 ITQCDIYSTLLGLPADIOAAQAMMVTSSAISLACIISVGMRCCTVCOESRAKORVAVA 120  
QY 121 GGVEFIIIGLGFIPVAMNHLGILRDFYSPVPDSMKFEIGEAALYDIIISLPSLGIIT 180  
Db 121 GGVEFIIIGLGFIPVAMNHLGILRDFYSPVPDSMKFEIGEAALYDIIISLPSLGIIT 180  
QY 181 LCFSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYSILGYV 230  
Db 181 LCFSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYSILGYV 230

## RESULT 3

US-09-663-600A-92  
Sequence 92, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bouguetieret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 92  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -24..-1  
NAME/KEY: UNSURE  
LOCATION: 54..79  
OTHER INFORMATION: Xaa = any one of the twenty amino acids  
US-09-663-600A-92

Query Match 55.2%; Score 127; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3.7e-111;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 CTYFCQESRAKORVAVAGVFFIIGLGFIPVAMNHLGILRDFYSPVPDSMKFEIGEA 163  
Db 104 CTYFCQESRAKORVAVAGVFFIIGLGFIPVAMNHLGILRDFYSPVPDSMKFEIGEA 163  
QY 164 LVYGIISLPSLGIITLFCSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYS 223  
Db 164 LVYGIISLPSLGIITLFCSCSSQRNRSNYYDAYOAOPLATRSSPRPGQPKYSEFNYS 223  
QY 224 YSLTGYV 230  
Db 224 YSLTGYV 230

## RESULT 4

US-09-282-029A-7  
Sequence 7, Application US/09282029A  
Patent No. 6723700  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
FILTRATION  
FILE REFERENCE: 100086,409C1  
CURRENT APPLICATION NUMBER: US/09/282,029A  
CURRENT FILING DATE: 1999-03-30  
NUMBER OF SEQ ID NOS: 480  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 7  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-282-029A-7

Query Match 16.5%; Score 38; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.1e-28;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TSSYVGASIVTAVGFSKGLMECATHTSGITQCDIYST 69

Db 5 TSSYVGASIVTAVGFSKGLMECATSTGTTCDDYST 42

RESULT 5  
US-09-185-908-7  
Sequence 7, Application US/09185908A  
Patent No. 6756356  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
APPLICANT: Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED  
TITLE OF INVENTION: FUNCTIONS  
FILE REFERENCE: 100086.409  
CURRENT APPLICATION NUMBER: US/09/185.908A  
CURRENT FILING DATE: 1998-11-03  
NUMBER OF SEQ ID NOS: 269  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-185-908-7

Query Match 16.5%; Score 38; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.1e-28;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TSSYVGASIVTAVGFSKGLMECATSTGTTCDDYST 69  
Db 5 TSSYVGASIVTAVGFSKGLMECATSTGTTCDDYST 42

RESULT 6  
US-09-252-991A-22641  
Sequence 22641, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22641  
LENGTH: 208  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22641

Query Match 3.9%; Score 9; DB 4; Length 208;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 ATRSSPPG 212  
Db 20 ATRSSPPG 28

RESULT 7  
US-08-525-539A-34  
Sequence 34, Application US/0855539A  
Patent No. 630636  
GENERAL INFORMATION:  
APPLICANT: DO COUTO, FERNANDO J.R.  
APPLICANT: CERIANI, ROBERTO L.  
APPLICANT: PETERSON, JERRY A.  
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525.539A  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DYLAN, TYLER  
REGISTRATION NUMBER: 37,612  
REFERENCE/DOCKET NUMBER: 27633-20001.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-525-539A-34

Query Match 3.5%; Score 8; DB 3; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GTIVAMLL 27  
Db 17 GTIVAMLL 24

RESULT 8  
US-09-275-252A-32  
Sequence 32, Application US/09275252A  
Patent No. 6641997  
GENERAL INFORMATION:  
APPLICANT: Mackinnon, Roderick  
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With  
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation  
FILE REFERENCE: 018512-002901US  
CURRENT APPLICATION NUMBER: US/09/275.252A  
CURRENT FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: US 09/045,529  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: US 09/054,347  
PRIOR FILING DATE: 1998-04-02  
PRIOR APPLICATION NUMBER: WO PCT/US99/06307  
PRIOR FILING DATE: 1999-03-22  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-275-252A-32

Query Match 3.5%; Score 8; DB 4; Length 58;  
Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 123 VFPIIGSL 130  
|||||  
DB 33 VFPIIGSL 40

RESULT 9  
US-09-252-991A-16828  
; Sequence 16828, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 16828  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16828

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 138;  
Pred. No. 8.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LGLPADI 77  
|||||  
DB 73 LGLPADI 80

RESULT 10  
US-09-248-796A-17661  
; Sequence 17661, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248.796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 17661  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (33)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno  
US-09-248-796A-17661

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 335;  
Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 PLATRSSP 209  
|||||  
DB 38 PLATRSSP 45

RESULT 11  
US-09-190-965-3  
; Sequence 3, Application US/09190965  
; Patent No. 6071721  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Gorgone, Gina A.  
; TITLE OF INVENTION: CALCIUM BINDING PROTEIN  
; FILE REFERENCE: PF-0635 US  
; CURRENT APPLICATION NUMBER: US/09/190,965  
; CURRENT FILING DATE: 1998-11-13  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: g262934  
US-09-190-965-3

Query Match  
Best Local Similarity 100.0%; Score 8; DB 3; Length 341;  
Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGTLVA 24  
|||||  
DB 78 GLGTLVA 85

RESULT 12  
US-09-470-253-3  
; Sequence 3, Application US/09470253  
; Patent No. 6365371  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Gorgone, Gina A.  
; TITLE OF INVENTION: CALCIUM BINDING PROTEIN  
; FILE REFERENCE: PF-0635 US  
; CURRENT APPLICATION NUMBER: US/09/470,253  
; CURRENT FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: 09/190,965  
; PRIOR FILING DATE: 1998-11-13  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: g262934  
US-09-470-253-3

Query Match  
Best Local Similarity 100.0%; Score 8; DB 3; Length 341;  
Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGTLVA 24  
|||||  
DB 78 GLGTLVA 85

RESULT 13  
US-09-252-991A-28079  
; Sequence 28079, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 31142  
SEQ ID NO 28079  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28079

Query Match 3.5%; Score 8; DB 4; Length 487;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 ILGLGL 82  
DB 294 ADIQAQA 301

RESULT 14  
US-09-091-725-13  
Sequence 13, Application US/09091725  
Patent No. 6329141  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Improved methods for transforming Phaffia  
TITLE OF INVENTION: and recombinant DNA for use therein  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 2000 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/091,725  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95203620.0  
FILING DATE: 22-DEC-1995  
APPLICATION NUMBER: EP 96200943.7  
FILING DATE: 11-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: E. Victor Donahue  
REGISTRATION NUMBER: 35,492  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-091-725-13

Query Match 3.5%; Score 8; DB 3; Length 673;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 ILGLGL 19  
DB 17 ILGLGL 24

RESULT 15  
US-09-091-725-19  
Sequence 19, Application US/09091725  
Patent No. 6329141  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Improved methods for transforming Phaffia  
TITLE OF INVENTION: and recombinant DNA for use therein  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster LLP  
STREET: 2000 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/091,725  
FILING DATE: 23-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95203620.0  
FILING DATE: 22-DEC-1995  
APPLICATION NUMBER: EP 96200943.7  
FILING DATE: 11-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: E. Victor Donahue  
REGISTRATION NUMBER: 35,492  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-091-725-19

Query Match 3.5%; Score 8; DB 3; Length 673;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 ILGLGL 19  
DB 17 ILGLGL 24

Search completed: October 27, 2004, 07:40:35  
Job time : 42 secs



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# OM protein - protein search, using sw model

Run on: October 27, 2004, 07:22:43 : Search time 38 Seconds  
(without alignments)  
582.365 Million cell updates/sec

Title: US-09-787-677A-3  
Perfect score: 230  
Sequence: 1 MASLGLVGYILGILGLG.....PGQPKVKSSEFNSYLTGVY 230

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	3.9	123	2	C87698 conserved hypotet
2	8	3.5	29	2	A53145 high conductance c
3	8	3.5	120	2	S21667 ig kappa chain V r
4	8	3.5	120	2	S21666 ig kappa chain V r
5	8	3.5	204	2	T45270 superoxide dismuta
6	8	3.5	215	2	AD0056 probable phosphogl
7	8	3.5	296	2	A70427 conserved hypotet
8	8	3.5	300	2	T32665 hypotetrical prote
9	8	3.5	323	2	B83215 conserved hypotet
10	8	3.5	341	2	I57997 hypotetrical calci
11	8	3.5	362	2	A31962 hypotetrical prote
12	8	3.5	404	1	G70151 pteromone shutoff
13	8	3.5	556	2	S02154 NADH2 dehydrogenas
14	8	3.5	609	2	I38586 calcium-activated
15	8	3.5	959	2	T25704 hypotetrical prote
16	8	3.5	1113	2	S62904 calcium-regulated
17	8	3.5	1184	2	I49017 calcium-activated
18	8	3.5	1196	2	A48206 calcium-activated
19	7	3.0	57	2	R35057 MHC class II histo
20	7	3.0	57	2	D35057 MHC class II histo
21	7	3.0	66	2	AH0823 conserved hypotet
22	7	3.0	66	2	F91052 hypotetrical prote
23	7	3.0	66	2	A84408 hypotetrical prote
24	7	3.0	66	2	B85897 hypotetrical prote
25	7	3.0	66	2	C65029 hypotetrical 7.7 k
26	7	3.0	68	2	S78739 protein YOL077w-a
27	7	3.0	82	2	I37070 gene MHC DQ-beta 1
28	7	3.0	90	2	G42518 structural protein
29	7	3.0	90	2	F36849 A1L protein - var

30	7	3.0	90	2	T28556 hypothetical prote
31	7	3.0	90	2	D72165 A1SL protein - var
32	7	3.0	92	2	S37531 ig kappa chain V r
33	7	3.0	94	2	A83523 hypotetrical prote
34	7	3.0	95	2	B81337 probable membrane
35	7	3.0	97	2	T34765 small hydrophobic
36	7	3.0	102	1	NRPLTB ribonuclease T1 (E
37	7	3.0	109	1	KVRB37 ig kappa chain V r
38	7	3.0	111	1	KVM869 ig kappa chain V r
39	7	3.0	113	2	S30520 ig kappa chain V r
40	7	3.0	128	2	H72500 hypotetrical prote
41	7	3.0	132	2	S46373 ig kappa chain V-J
42	7	3.0	160	1	S16918 plastoquinol-plast
43	7	3.0	177	2	G75285 hypotetrical prote
44	7	3.0	184	2	H84780 probable AP2 domai
45	7	3.0	184	2	A37041 homeotic protein A

## ALIGNMENTS

RESULT 1  
C87698 conserved hypothetical protein CC3621 [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #ext\_change 09-Jul-2004  
C/Accession: C87698  
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gattm, M.L.; Hart, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; NCID:21173698; PMID:11259647  
A/Accession: C87698  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-123 <STO>  
A/Cross-references: UNIPROT:Q9A284; GB:AE005673; NID:G13425371; PIDN:AAK25583.1; GSPDB:GT  
C/Genetics:  
A/Genes: CC3621

Query Match 3.9%; Score 9; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 0.45;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VFPIIGGL 131  
Db 27 VFPIIGGL 35

RESULT 2  
A53145 high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #ext\_change 09-Jul-2004  
C/Accession: A53145  
R/Klaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.  
J. Biol. Chem. 269, 3921-3924, 1994  
A/Title: Subunit composition of the high conductance calcium-activated potassium channel  
A/Reference number: A53145; NCID:94140798; PMID:7508434  
A/Accession: A53145  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-29 <RNA>  
A/Cross-references: UNIPROT:Q9TS86  
A/Note: sequence extracted from NCBI backbone (NCBI:144545)  
C/Superfamily: fruit fly calcium-activated potassium channel s10

Query Match 3.5%; Score 8; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 123 VFPIIGGL 130

Db 9 VFFPLGL 16

## RESULT 3

S21667  
Ig kappa chain V region (23) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S21667  
R/Roeschenthaler, F.; Schaeble, K.F.; Thiebe, R.; Zachau, H.G.  
Biol. Chem. Hoppe-Seyler 373, 177-186, 1992  
A/Title: Of orphans and UHOS. Delimitation of the germline repertoire of human immunoglobulin  
A/Reference number: S21666; MUID:92281681; PMID:1596359  
A/Accession: S21667  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-120 <ROE>  
A/Cross-references: EMBL:X64641  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/41-115/Domain: immunoglobulin homology <IMM>

Query Match 3.5%; Score 8; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGHLGLG 20  
Db 10 LGHLGLG 17

## RESULT 4

S21666  
Ig kappa chain V region (22) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C/Accession: S21666  
R/Roeschenthaler, F.; Schaeble, K.F.; Thiebe, R.; Zachau, H.G.  
Biol. Chem. Hoppe-Seyler 373, 177-186, 1992  
A/Title: Of orphans and UHOS. Delimitation of the germline repertoire of human immunoglobulin  
A/Reference number: S21666; MUID:92281681; PMID:1596359  
A/Accession: S21666  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-120 <ROE>  
A/Cross-references: EMBL:X64640; NID:9432649; PIDN:CAA45914.1; PID:G1335149  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/41-115/Domain: immunoglobulin homology <IMM>

Query Match 3.5%; Score 8; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LGHLGLG 20  
Db 10 LGHLGLG 17

## RESULT 5

T45270  
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Thermus aquaticus  
N/Alternate names: manganese superoxide dismutase  
C/Species: Thermus aquaticus  
C/Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T45270  
R/Motochima, H.; Minagawa, E.; Tsukaaki, F.; Kamimogawa, S.  
J. Ferment. Bioeng. 86, 21-27, 1998  
A/Title: Cloning and nucleotide sequencing of genes encoding Mn-superoxide dismutase and  
A/Reference number: Z22952  
A/Accession: T45270  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-204 <MOT>  
A/Cross-references: UNIPROT:P53653; EMBL:DB4646; PIDN:BAAL2703.1  
A/Experimental source: strain YT-1  
C/Superfamily: superoxide dismutase (Mn)  
C/Keywords: manganese; metalloprotein; oxidoreductase  
F/29,84,167,171/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 3.5%; Score 8; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 LPADIQAA 80  
Db 66 LPADIQAA 73

## RESULT 6

AD0056  
Probable phosphoglycerate mutase (EC 5.4.2.1) [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 16-Aug-2004  
C/Accession: AD0056  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AD0056  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-215 <RUR>  
A/Cross-references: UNIPROT:Q8Z1P0; GB:AL590842; PIDN:CAC89311.1; PID:G15978547; GSPDB:GP  
C/Genetics:  
A/Genes: gpmB  
C/Superfamily: Cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol  
C/Keywords: Intramolecular transferase; isomerase

Query Match 3.5%; Score 8; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 STLGLPAA 75  
Db 159 STLGLPAA 166

## RESULT 7

A70427  
conserved hypothetical protein aq\_1462 - Aquifex aeolicus  
C/Species: Aquifex aeolicus  
C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C/Accession: A70427  
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove  
V.  
Nature 392, 353-358, 1998  
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A/Reference number: A70300; MUID:98196666; PMID:9537320  
A/Accession: A70427  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-236 <AQF>  
A/Cross-references: UNIPROT:O67443; GB:AE000741; NID:G2983841; PIDN:AAC07409.1; PID:G298;  
A/Experimental source: strain VFS  
C/Genetics:  
A/Genes: aq\_1462  
C/Superfamily: conserved hypothetical protein AF1561

Query Match 3.5%; Score 8; DB 2; Length 296;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 125 FIGGLIG 132  
 DB 84 FIGGLIG 91

## RESULT 8

T32665  
 hypothetical protein Fl6B4.6 - *Caenorhabditis elegans*  
 C/Species: *Caenorhabditis elegans*  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T32665  
 R/Davidson, S.; Mohldamm, P.; Bauer, C.; O'Neal, D.  
 submitted to the EMBL Data Library, December 1997  
 A/Description: The sequence of *C. elegans* cosmid Fl6B4.  
 A/Reference number: Z21208  
 A/Accession: T32665  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-300 <DAV>  
 A/Cross-references: UNIPROT:O44628; EMBL:AF039048; PIDD:AA94237.1; GSPDB:GN00023; CESP:  
 A/Experimental source: strain Bristol N2; clone Fl6B4  
 C/Genetics:  
 A/Map position: 5  
 A/Introns: 49/1; 128/2; 186/3; 241/3

Query Match 3.5%; Score 8; DB 2; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 8.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 VTSSA185 92  
 DB 178 VTSSA185 185

RESULT 9  
 B83215  
 conserved hypothetical protein PA3445 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C/Species: *Pseudomonas aeruginosa*  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C/Accession: B83215  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.D.; Br  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 .; Lox, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-323 <STO>  
 A/Cross-references: UNIPROT:Q9HYG1; GB:AE004765; GB:AE004091; NID:G9949580; PIDD:AA00683  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Map position: 5  
 A/Introns: 49/1; 128/2; 186/3; 241/3

Query Match 3.5%; Score 8; DB 2; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 LGLPADI 77  
 DB 258 LGLPADI 265

RESULT 10  
 I57997  
 hypothetical calcium-binding protein - mouse  
 C/Species: *Mus sp.* (mouse)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
 C/Accession: I57997  
 R/Miyamoto, H.; Matsushiro, A.; Nozaki, M.  
 Mol. Reprod. Dev. 34, 1-7, 1993

A/Title: Molecular cloning of a novel mRNA sequence expressed in cleavage stage mouse emt  
 A/Reference number: I57997; MUID:93119656; PMID:8418809  
 A/Accession: I57997  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-341 <RES>  
 A/Cross-references: GB:851858; NID:G262933; PIDD:AA24801.1; PID:G262934  
 C/Superfamily: Saccharomycetes hypothetical protein YKL189w  
 C/Keywords: calcium binding

Query Match 3.5%; Score 8; DB 2; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 9.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGLTIVA 24  
 DB 78 GLGLTIVA 85

RESULT 11  
 AG1962  
 hypothetical protein alr1250 [imported] - *Nostoc* sp. (strain PCC 7120)

C/Species: *Nostoc* sp. PCC 7120  
 A/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C/Accession: AG1962  
 R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,  
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anat*  
 A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AG1962  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-362 <KUR>  
 A/Cross-references: UNIPROT:Q9YX33; GB:BA000019; PIDD:BB73207.1; PID:G17130597; GSPDB:G  
 A/Experimental source: strain PCC 7120  
 C/Genetics:  
 A/Map position: 5  
 A/Introns: 49/1; 128/2; 186/3; 241/3

Query Match 3.5%; Score 8; DB 2; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GLGLTIVA 24  
 DB 319 GLGLTIVA 326

RESULT 12  
 G70151  
 phenomone shutdown protein (trab) homolog - Lyme disease spirochete

C/Species: *Borrelia burgdorferi* (Lyme disease spirochete)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: G70151  
 R/Trasler, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,  
 son, D.; Peterson, J.; Keriavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horel, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997

A/Authors: Smith, H.O.; Venter, J.C.  
 A/Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.  
 A/Reference number: A70100; MUID:98065943; PMID:9403685  
 A/Accession: G70151  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-404 <LKB>  
 A/Cross-references: UNIPROT:O51377; GB:AE001146; GB:AE000783; NID:G2688312; PIDD:AA06678;  
 A/Experimental source: strain B31  
 C/Superfamily: phenomone shutdown protein

Query Match 3.5%; Score 8; DB 1; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 168 ISSLSFSL 175  
 |||||  
 Db 158 ISSLSFSL 165

## RESULT 13

S02154  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Podospora anserina mitochondrion  
 N:Alternate names: NADH-ubiquinone oxidoreductase chain 2  
 C:Species: mitochondrion Podospora anserina  
 C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
 C:Accession: S02154  
 R: Cummings, D.J.; Domenico, J.M.  
 J. Mol. Biol. 204, 815-839, 1988  
 A:Title: Sequence analysis of mitochondrial DNA from Podospora anserina. Pervasiveness  
 A:Reference number: S02153; PMID:89125610; PMID:2975708  
 A:Accession: S02154  
 A:Molecule type: DNA  
 A:Residues: 1-556 <CDM>  
 A:Cross-references: UNIPROT:P15578; EMBL:X14485; NID:G13296; PIDN:CAA32646.1; PID:G13297  
 C:Genetics:  
 A:Gene: ND2  
 A:Genome: mitochondrion  
 A:Genetic code: SGC3  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2  
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

## Query Match

3.5%; Score 8; DB 2; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ISSLSFSLI 176  
 |||||  
 Db 310 ISSLSFSLI 317

## RESULT 14

I38596  
 calcium-activated potassium channel - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C:Accession: I38596  
 R: Pallanck, L.; Ganetzky, B.  
 Hum. Mol. Genet. 3, 1239-1243, 1994  
 A:Title: Cloning and characterization of human and mouse homologs of the Drosophila calc  
 A:Reference number: I38415; PMID:95078823; PMID:7967297  
 A:Accession: I38596  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-609 <RES>  
 A:Cross-references: UNIPROT:Q12791; EMBL:U09384; NID:9487798; PIDN:AAA50216.1; PID:94935  
 C:Superfamily: fruit fly calcium-activated potassium channel s10

## Query Match

3.5%; Score 8; DB 2; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VPFILGSL 130  
 |||||  
 Db 305 VPFILGSL 312

## RESULT 15

T25704  
 hypothetical protein F18F11.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T25704  
 R: Du, Z.; Maggi, L.  
 submitted to the EMBL Data Library, February 1997  
 A:Description: The sequence of C. elegans cosmid F18F11.

A:Reference number: Z20072

A:Accession: T25704

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-959 <DUZ>

A:Cross-references: UNIPROT:P91263; EMBL:U88176; PIDN:AAA42287.1; GSPDB:GN00022; CESP:Fl

A:Experimental source: strain Bristol N2; clone F18F11

C:Genetics:

A:Gene: CESP:F18F11.4

A:Map position: 4

A:introns: 16/3; 75/3; 104/1; 188/3; 297/3; 361/1; 400/2; 435/3; 454/1; 540/2; 607/2; 688

## Query Match

3.5%; Score 8; DB 2; Length 959;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 AVAGGVFF 125  
 |||||  
 Db 334 AVAGGVFF 341

Search completed: October 27, 2004, 07:36:28  
 Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 27, 2004, 07:22:58 ; Search time 194 Seconds

(without alignments)  
682.145 Million cell updates/sec

Title: US-09-787-677A-3

Perfect score: 230

Sequence: 1 MSISGLVGYILGLGLG.....PGQPKVSEFNSYLTGYV 230

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	230	100.0	230	1	CLD2_HUMAN	P57739 homo sapien
2	230	100.0	230	2	BAC11575	Bac11575 homo sapi
3	230	100.0	230	2	AAH71747	Aah71747 homo sapi
4	59	25.7	230	2	Q765P1	Q765P1 bos taurus
5	59	25.7	230	2	BAD01111	Bad01111 bos tauru
6	58	25.2	230	1	CLD2_CANFA	Q95K66 canis fami1
7	58	25.2	230	1	CLD2_MOUSE	Q88552 mus musculu
8	58	25.2	230	2	BAB37325	Bab37325 mus muscu
9	3.9	3.9	123	2	Q9A2E4	Q9A2E4 caulobacter
10	3.9	3.9	297	2	Q7NDS4	Q7NDS4 glieobacter
11	3.9	3.9	307	2	Q9FKP4	Q9FKP4 arabidopsis
12	3.9	3.9	346	2	Q9NMY4	Q9NMY4 homo sapien
13	3.9	3.9	359	2	Q98189	Q98189 acrocephalu
14	3.9	3.9	359	2	Q98192	Q98192 acrocephalu
15	3.9	3.9	359	2	Q98193	Q98193 acrocephalu
16	3.9	3.9	360	2	Q98187	Q98187 acrocephalu
17	3.9	3.9	360	2	Q98188	Q98188 acrocephalu
18	3.9	3.9	360	2	Q98191	Q98191 acrocephalu
19	3.9	3.9	681	2	Q95RM4	Q95RM4 drosophila
20	3.9	3.9	930	2	Q74906	Q74906 geobacter s
21	3.9	3.9	930	2	AAR36058	Aar36058 geobacter
22	3.9	3.9	1406	2	Q9U110	Q9U110 drosophila
23	3.9	3.9	1406	2	Q9V4D4	Q9V4D4 drosophila
24	3.9	3.9	1408	2	Q9XZU7	Q9XZU7 drosophila
25	8	3.5	48	2	Q9TS86	Q9TS86 bos taurus
26	8	3.5	100	2	Q8K16	Q8K16 pseudomonas
27	8	3.5	127	2	Q84NR7	Q84NR7 oryza sativ
28	8	3.5	140	2	Q9KMR7	Q9KMR7 pseudomonas
29	8	3.5	140	2	Q9KMR7	Q9KMR7 pseudomonas
30	8	3.5	140	2	Q9KHS0	Q9KHS0 pseudomonas
31	8	3.5	152	1	EXBB_PASHA	P72202 pasteurella

32	8	3.5	203	1 SODM_THEAQ	P53653 thermus aqu
33	8	3.5	205	2 Q83C97	Q83C97 coxiella bu
34	8	3.5	215	1 Q8Z10 YERSINA PE	Q8Z10 yersinia pe
35	8	3.5	233	1 AMP_ONYPE	Q7mit6 onion yello
36	8	3.5	233	2 Q9A1R8	Q9A1R8 aster yello
37	8	3.5	246	2 Q44630	Q44630 caenorhabdi
38	8	3.5	282	2 Q89RN4	Q89rn4 bradyrhizob
39	8	3.5	288	2 Q72WQ8	Q72wq8 desulfocivib
40	8	3.5	288	2 AAS94419	Aas94419 desulfovi
41	8	3.5	292	2 Q7QW15	Q7qwt5 anopheles g
42	8	3.5	296	2 Q67443	Q67443 aquifer aco
43	8	3.5	296	2 Q73DC8	Q73dc8 bacillus ce
44	8	3.5	296	2 AAS39717	Aas39717 bacillus
45	8	3.5	311	2 Q88TD9	Q88td9 lactobacilli

#### ALIGNMENTS

RESULT 1  
CLD2\_HUMAN STANDARD; PRT; 230 AA.  
ID P57739;  
AC P57739;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Claudin-2 (UNQ705/PRO1356) (SP82).  
GN Name=CLDN2;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Epithelium;  
RA Reinacker H.-C., Sakaguchi T., Golden H.M.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clones with function of inhibiting cancer cell  
RT growth."  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Lao D., Mark M., Robble E., Sanchez C., Schenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,  
RA Wadlen R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment."  
RL Genome Res. 13:1265-2270(2003).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Heath P.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon, and Kidney;  
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Krausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,



RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.

RC TISSUE=skin and meninges pool - skin;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC071747; AAH71747.1; -  
 SQ SEQUENCE 230 AA; 24548 MW; 52CA642D4A62B70D CRC64;

Query Match 100.0%; Score 230; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 66-215;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLVGYILGLLGLTLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 DB 1 MASLGLVGYILGLLGLTLVAMLLPSWKTSSVYGASIVTAVGFSKGLMECATHTSG 60  
 QY 61 ITQCDIYSTLGLPADIOAAQAMWVTSSAISLACTIISVGMKCTVPCQESRAKRVAVA 120  
 DB 61 ITQCDIYSTLGLPADIOAAQAMWVTSSAISLACTIISVGMKCTVPCQESRAKRVAVA 120  
 QY 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 180  
 DB 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 180  
 QY 181 LCFSSCSQRNSRYDAYOQAPLATRSSPRPGOPPKVSEFNSYSLTGYV 230  
 DB 181 LCFSSCSQRNSRYDAYOQAPLATRSSPRPGOPPKVSEFNSYSLTGYV 230

RESULT 4  
 ID 076SP1 PRELIMINARY; PRT; 230 AA.

AC 076SP1  
 DT 05-JUL-2004 (TEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
 DE Claudin 2.  
 GN Name=CLDN2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ohta H., Takiguchi M., Inaba M.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB115779; BAB01111.1; -  
 DR InterPro: IPR006187; Claudin.  
 DR InterPro: IPR005411; Claudin2.  
 DR InterPro: IPR006188; Claudin\_reg.  
 DR Pfam: PF00822; PMP22 Claudin.  
 DR PRINTS: PRO1077; CLAUDIN.  
 DR PRINTS: PRO1589; CLAUDIN2.  
 DR PROSITE: PS01346; CLAUDIN.1.  
 KW Transmembrane.  
 SQ SEQUENCE 230 AA; 24533 MW; ED241778B0B541CA CRC64;

Query Match 25.7%; Score 59; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 179  
 DB 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 179

RESULT 5  
 ID BAD01111 PRELIMINARY; PRT; 230 AA.

AC BAD01111  
 DT 02-MAR-2004 (TEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)  
 DE Claudin 2.  
 GN CLDN2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Ohta H., Takiguchi M., Inaba M.;  
 RL "Localization of claudin proteins in bovine kidneys.";  
 DR EMBL: AB115779; BAB01111.1; -  
 SQ SEQUENCE 230 AA; 24533 MW; ED241778B0B541CA CRC64;

Query Match 25.7%; Score 59; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-48;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 179  
 DB 121 GGVPFLIGLGLRIPVAMNHLGILRDFYSPVDPDSMKFEIGALYIGIISLPSLIAGI 179

RESULT 6  
 ID CLD2\_CANFA STANDARD; PRT; 230 AA.

AC 095KM6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Claudin-2.  
 GN Name=CLDN2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=21206012; PubMed=11309408;  
 RA Furness M., Furness K., Sasaki H., Teukila S.;  
 RT "Conversion of zonulae occludentes from tight to leaky strand type by  
 RT introducing claudin-2 into Madin-Darby canine kidney I cells.";  
 RL J. Cell Biol. 153:263-272(2001).  
 CC -1- FUNCTION: Component of tight junction (TJ) strands.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the claudin family.

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 CC -----  
 CC EMBL: AF389807; AKS51433.1; -  
 DR InterPro: IPR006187; Claudin.  
 DR InterPro: IPR005411; Claudin2.  
 DR InterPro: IPR006188; Claudin\_reg.  
 DR InterPro: IPR004031; PMP22 Claudin.  
 DR Pfam: PF00822; PMP22\_Claudin.1.

DR PRINTS; PRO1077; CLAUDIN.  
DR PRINTS; PRO1589; CLAUDIN2.  
DR PROSITE; PS01346; CLAUDIN.1.  
KW Tight junction; Transmembrane.  
FT TRANSMEM 8 28 Potential.  
FT TRANSMEM 82 102 Potential.  
FT TRANSMEM 117 137 Potential.  
FT TRANSMEM 163 183 Potential.  
SQ SEQUENCE 230 AA; 24502 MW; 91B7LCIE5CDC4BB9 CRC64;

Query Match 25.2%; Score 58; DB 1; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-47;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

39 SITVANGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSAISLACI 96  
39 SITVANGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSAISLACI 96

RESULT 7  
CLD2\_MOUSE STANDARD; PRT; 230 AA.  
AC 088552;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Claudin-2.  
GN Name=Cldn2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98311639; PubMed=9647647;  
RA Furness M., Fujita K., Hiltag T., Fujimoto K., Tsukita S.;  
RT "Claudin-1 and -2: novel integral membrane proteins localizing at  
tight junctions with no sequence similarity to occludin.";  
RL J. Cell Biol. 141:1539-1550(1998).  
CC -1- FUNCTION: Component of tight junction (TJ) strands.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to the claudin family.  
-----  
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CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
-----  
CC EMBL; AF072128; AAC27079.1; -  
DR MGD; MG11276110; Cldn2.  
DR InterPro; IPR006187; Claudin.  
DR InterPro; IPR005411; Claudin.  
DR InterPro; IPR006188; Claudin2.  
DR InterPro; IPR004031; PMP22 Claudin.  
DR Pfam; PF00822; PMP22 Claudin; 1.  
DR PRINTS; PRO1077; CLAUDIN.  
DR PRINTS; PRO1589; CLAUDIN2.  
DR PROSITE; PS01346; CLAUDIN.1.  
KW Tight junction; Transmembrane.  
FT TRANSMEM 8 28 Potential.  
FT TRANSMEM 82 102 Potential.  
FT TRANSMEM 117 137 Potential.  
FT TRANSMEM 163 183 Potential.  
SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match 25.2%; Score 58; DB 1; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.1e-47;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

32 TSSVGAISVTAVGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSA 89

Db 32 TSSVGAISVTAVGFSKGLMECATHTSTGTCDDIYSTLLGLPADIOAQAQMMVTSSA 89

RESULT 8  
BAB3725 PRELIMINARY; PRT; 230 AA.  
ID BAB3725;  
AC BAB3725;  
DT 14-APR-2004 (TrEMBLrel. 27, Created)  
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Adult male liver cDNA, RIKEN full-length enriched library,  
clone:1300013G06 product:claudin 2, full insert sequence.  
DE clone:1300013G06 product:claudin 2, full insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=21085660; PubMed=11217651;  
RA RIKEN FANTOM Consortium,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Mech. Enzymol. 303:19-44(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama Y., Nishi K., Kikunishi T., Taisho H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Washiwaki K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arawaka T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kuribara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK004990; BAB23725.1; -  
 SQ SEQUENCE 230 AA; 24483 MW; 38A7C074A1E0D5D2 CRC64;

Query Match 25.2%; Score 58; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-47;  
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TSSYVGSIVTAVGFSKGLMMECATHTSTGTCCDIYSTLLGLPADIQAAQAMVVTSSA 89  
 DB 32 TSSYVGSIVTAVGFSKGLMMECATHTSTGTCCDIYSTLLGLPADIQAAQAMVVTSSA 89

RESULT 9  
 Q9A2E4 PRELIMINARY; PRT; 123 AA.  
 AC 09A2E4;  
 DT 01-JUN-2001 (TEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein CC3621.  
 GN OrderedLocustNames=CC3621;  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
 OC Caulobacteraceae; Caulobacter.  
 NCBI\_TaxID=155892;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173658; PubMed=11259647; DOI=10.1073/pnas.061029298;  
 RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,  
 RA Berry K.J., Ueberbach T.R., Tran K., Wolf A.M., Vamathevan J.J.,  
 RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL: AEO06020; AAK25583.1; -  
 DR PIR: C87698; C87698.  
 DR TIGR: CC3621; -  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR InterPro: IPR003425; Unk\_YGGR.  
 DR Pfam: PF02325; YGGR; 1..YGGR.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 123 AA; 13427 MW; 15F76F23C280DAC2 CRC64;

Query Match 3.9%; Score 9; DB 2; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 VFFILGGL 131  
 DB 27 VFFILGGL 35

RESULT 10  
 Q7ND54 PRELIMINARY; PRT; 297 AA.  
 AC Q7ND54;  
 DT 01-MAR-2004 (TEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE G1r4158 protein.  
 GN OrderedLocustNames=g1r4158;  
 OS Gloeobacter violaceus.  
 OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.

OX NCBI\_TaxID=33072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7421.  
 RX MEDLINE=22977040; PubMed=14621292;  
 RA Nakamura Y., Kaneko T., Sato S., Muro M., Miyashita H., Tsuchiya T.,  
 RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,  
 RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a  
 cyanobacterium that lacks thylakoids.";  
 RL DNA Res. 10:137-145(2003).  
 DR EMBL: AP006582; BAC92099.1; -  
 DR InterPro: IPR001279; Blactamase-like.  
 DR Pfam: PF00753; Lactamase\_B; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 297 AA; 33846 MW; 720044C2AD2AAE4B CRC64;

Query Match 3.9%; Score 9; DB 2; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 PADIQAAQA 82  
 DB 76 PADIQAAQA 84

RESULT 11  
 Q9FKF4 PRELIMINARY; PRT; 307 AA.  
 AC Q9FKF4;  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)  
 DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1109  
 GN (Hypothetical protein At5g61670) (AT5g61670/k1109\_190).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98403884; PubMed=9734815;  
 RA Kocani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and TAC clones.";  
 RL DNA Res. 5:203-216(1998).  
 [2]

RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
 RA Gerninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 [3]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22088475; PubMed=12093376;  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,  
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
 RT "Full-length messenger RNA sequences greatly improve genome  
 RT annotation.";  
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.,



RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyere M.C., Banh J.,  
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlín-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
 RA Deng C., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L.,  
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlín-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Bower L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,  
 RA Heuan V.W., Ishida J., Jones T., Kamiya A., Karlín-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,  
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,  
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP EMBL: AB012339; BAB09011.1; -  
 DR EMBL: AY065401; BAB38842.1; -  
 DR EMBL: AY084568; AAM61134.1; -  
 DR EMBL: AY094431; AAM19804.1; -  
 DR EMBL: AY117226; AAM51301.1; -  
 DR EMBL: AY149953; AAN31107.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 307 AA; 33789 MW; CB0C55C0C7CD80BA CRC64;  
 QY Query Match 3.9%; Score 9; DB 2; Length 307;  
 Db Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 173 FSLIAGIIL 181  
 Db 152 FSLIAGIIL 160  
 RESULT 12  
 ID 09NMW4 PRELIMINARY; PRT; 346 AA.  
 AC 09NMW4;  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein FLJ20534 (Hypothetical protein  
 DE DKFZ564H1372).  
 GN Name=FLJ20534; Synonyms=DKFZ564H1372;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
 RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,  
 RA Nakamura Y., Iwagaki T., Sugano S., Iehara T., Tanaka T.,  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caeswain T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Blum H., Baerachis S., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK000541; BAA91241.1; -  
 DR EMBL: BC010367; AAI10367.1; -  
 DR EMBL: AL136673; CAB66608.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 346 AA; 39408 MW; 6089FF0759CEB50B CRC64;  
 QY Query Match 3.9%; Score 9; DB 2; Length 346;  
 Db Best Local Similarity 100.0%; Pred. No. 7.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ASLGLQLVG 10  
 Db 74 ASLGLQLVG 82  
 RESULT 13  
 ID 098189 PRELIMINARY; PRT; 359 AA.  
 AC 098189;  
 DT 01-MAY-1999 (TEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE MHC class I antigen.  
 OS Acropetalus arundinaceus (great reed warbler).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sylvidae; Acropetalus.  
 OX NCBI\_TaxID=39621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=99115500; PubMed=9914330;  
 RA Westerdahl H., Wittzell H., von Schantz T.,  
 RT "Polymorphism and transcription of Mhc class I genes in a passerine  
 RT bird, the great reed warbler.";  
 RL Immunogenetics 49:158-170 (1999).  
 DR EMBL: AU005505; CAA06562.1; -  
 DR HSP: 09HC68; 1A6Z.  
 DR GO: GO:0016020; C-membrane; IEA.  
 DR GO: GO:0006955; P-immune response; IEA.  
 DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam: PF07654; Cl-set; 1.  
 DR Pfam: PF00129; MHC\_I; 1.  
 DR PRINTS: PR01638; MHCCLASSI.  
 DR ProDom: PD000050; MHC\_I; 1.  
 DR SMART: SM00407; IgC1; 1.  
 DR PROSITE: PS00835; Ig\_LIKE; 1.  
 DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 359 AA; 4004 MW; 1C3E9C425A68B50 CRC64;

Query Match 3.9%; Score 9; DB 2; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILGLGLG 20  
 DB 10 ILGLGLG 18

RESULT 14  
 098192 PRELIMINARY; PRT; 359 AA.  
 AC 098192;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE MHC class I antigen.  
 OS Acrocephalus arundinaceus (great reed warbler).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.  
 OX NCBI\_TaxID=39621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=99115500; PubMed=9914330;  
 RA Westerdahl H., Witzell H., von Schantz T.;  
 RT "Polymorphism and transcription of Mhc class I genes in a passerine  
 bird, the great reed warbler.";  
 RL Immunogenetics 49:158-170(1999).  
 DR EMBL; AJ005508; CAA06565.1; -.  
 DR HSP; O9HC68; 1A6Z.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0006955; P-immune response; IEA.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IgC1; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 359 AA; 4038 MW; 0563362BP17D6B9 CRC64;

Query Match 3.9%; Score 9; DB 2; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILGLGLG 20  
 DB 10 ILGLGLG 18

RESULT 15  
 098193 PRELIMINARY; PRT; 359 AA.  
 AC 098193;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE MHC class I antigen.  
 OS Acrocephalus arundinaceus (great reed warbler).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Sylviidae; Acrocephalus.  
 OX NCBI\_TaxID=39621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=99115500; PubMed=9914330;  
 RA Westerdahl H., Witzell H., von Schantz T.;  
 RT "Polymorphism and transcription of Mhc class I genes in a passerine  
 bird, the great reed warbler.";  
 RL Immunogenetics 49:158-170(1999).  
 DR EMBL; AJ005509; CAA06566.1; -.  
 DR HSP; O9HC68; 1A6Z.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0006955; P-immune response; IEA.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IgC1; 1.  
 DR PROSITE; PS00835; Ig\_LIKE; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 359 AA; 39921 MW; 61484572AEXC8D6A CRC64;

Query Match 3.9%; Score 9; DB 2; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILGLGLG 20  
 DB 10 ILGLGLG 18

Search completed: October 27, 2004, 07:39:49  
 Job time: 196 secs

